

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 03:14:08 ; Search time 7483 Seconds
(without alignments)
4118.337 Million cell updates/sec

Title: US-10-088-950A-1

Perfect score: 3498

Sequence: 1 MRGRGAPFWLWPLKALL.....FLTPPELGLGPPRPOVLA 636

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3498	100.0	2646	6 AX114318	AX114318 Sequence
3	3498	100.0	2663	6 AR022524	AR022524 Sequence
4	3498	100.0	2663	6 AR099897	AR099897 Sequence

ALIGNMENTS

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VERSION	BC028003.1	GI:20380120					
KEYWORDS	MGC.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 2438)						
AUTHORS	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy J.J., Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D.,						

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2438)
Strausberg, R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.ncgcnhri.nih.gov
Akhtar, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bonifard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Guffard, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, O.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgueon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Query Match: 100.00% Indels: 0
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RESULT 2

AX114318

LOCUS AX114318 2646 bp DNA linear PAT 11-MAY-2001

DEFINITION Sequence 3 from Patent WO0129070.

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VERSION AX114318.1 GI:14031282
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 de Sauvage, F.J., Grewal, I. and Gurney, A.L.
 AUTHORS Type I cytokine receptor tccr
 TITLE Patent: WO 0129070-A 3 26-APR-2001;
 JOURNAL Genentech, Inc. (US)
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ACCESSION AR022524
VERSION AR022524.1 GI:3976586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2663)
AUTHORS Baumgartner, J.W., Foster, D.C., Grant, F.J. and Sprecher, C.A.
TITLE Hematopoietic cytokine receptor
JOURNAL Patent: US 5792850-A 4 11-AUG-1998;
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VERSION AR099897.1 GI:12810345
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2663)
AUTHORS Baumgartner,J.W., Foster,D.C., Grant,F.J. and Sprecher,C.A.
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JOURNAL Patent: US 6080406-A 4 27-JUN-2000;
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US-10-088-950A-1 (1-636) x AF053004 (1-2663)

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1 (bases 1 to 2677)
AUTHORS Zhang, W., Wan, T., He, L., Yuan, Z. and Cao, X.
TITLE A novel gp130-like cytokine receptor
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 2677)
AUTHORS Zhang, W., Wan, T., He, L., Yuan, Z. and Cao, X.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1998) Department of Immunology, Shanghai
Brilliance Biotechnology Institute & Second Military Medical
University, 800 Xiangyin Road, Shanghai 200433, P.R. China
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US-10-088-950A-1 (1-636) x AF106912 (1-2677)

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 VERSION AF265242.1 GI:11036791
 KEYWORDS
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2628)
 Chen, Q., Ghilardi, N., Wang, H., Baker, T., Xie, M. H., Gurney, A.,
 Grewal, I. S. and de Sauvage, F. J.
 Development of Th1-type immune responses requires the type I
 cytokine receptor TCCR
 JOURNAL Nature 407 (6806), 916-920 (2000)
 MEDLINE 20509354
 PUBMED 11057672
 REFERENCE 2 (bases 1 to 2628)
 AUTHORS Chen, Q., Ghilardi, N., Wang, H., Xie, M. H., Gurney, A., Grewal, I. S.

and de Sauvage, F. J.
 Direct Submission
 Submitted (08-MAY-2000) Molecular Oncology, Genentech Inc., 1 DNA
 Way, South San Francisco, CA 94080, USA

FEATURES
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ACCESSION AY358876
VERSION AY358876.1 GI:37182869
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2646)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Curreli,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
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Stinson,J., Vagts,A., Vandlen,K., Watanabe,C., Wiand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
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JOURNAL

PUBMED

REFERENCE

2 (bases 1 to 2646)

Clark,H.F.

Direct Submission

TITLE

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,

Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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US-10-088-950A-1 (1-636) x AY358876 (1-2646)

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REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 8965 06-SEP-2002;
PE Corporation (NY) (US)
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ACCESSION AR022523
VERSION AR022523.1 GI:3976585
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2368)
AUTHORS Baumgartner,J.W., Foster,D.C., Grant,F.J. and Sprecher,C.A.
TITLE Hematopoietic cytokine receptor
JOURNAL Patent: US 5792850-A 2 11-AUG-1998;
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US-10-088-950A-1 (1-636) x AR022523 (1-2368)
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ACCESSION  AR099896
VERSION     AR099896.1  GI:12810344
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 2368)
AUTHORS     Baumgartner,J.W., Foster,D.C., Grant,F.J. and Sprecher,C.A.
TITLE       Hematopoietic cytokine receptor
JOURNAL     Patent: US 6080406-A 2 27-JUN-2000;
FEATURES    Location/Qualifiers
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Percent Similarity: 90.88%      Conservative: 0
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SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2586)
AUTHORS Sprechter,C.A., Grant,F.J., Baumgartner,J.W., Presnell,S.R.,
Schrader,S.K., Yamagiwa,T., Whitmore,T.E., O'Hara,P.J. and
Foster,D.F.
TITLE Cloning and characterization of a novel class I cytokine receptor
JOURNAL Biochem. Biophys. Res. Commun. 246 (1), 82-90 (1998)
MEDLINE 98262921
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REFERENCE 2 (bases 1 to 2586)
AUTHORS Sprechter,C.A., Grant,F.J., Baumgartner,J.W., Presnell,S.R.,
Schrader,S.K., Yamagiwa,T., Whitmore,T.E., O'Hara,P.J. and
Foster,D.F.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-1998) Biomedical Informatics, ZymoGenetics,
Inc., 1201 Eastlake Ave. E., Seattle, WA 98102, USA
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Alignment Scores:

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 01:39:23 ; Search time 894 Seconds
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_16Dec04 -QMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloms62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: Geneseq_16Dec04:*
2: Geneseq_1980s:*
3: Geneseq_1990s:*
4: Geneseq_2000s:*
5: Geneseq_2001as:*
6: Geneseq_2002as:*
7: Geneseq_2002bs:*
8: Geneseq_2003as:*
9: Geneseq_2003bs:*
10: Geneseq_2003cs:*
11: Geneseq_2003ds:*
12: Geneseq_2004as:*
13: Geneseq_2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	2646	4 AAS03262	Aas03262 Human cdn
2	3498	100.0	2657	10 ADD88150	Add88150 Human WSX
3	3498	100.0	2657	11 ADL26573	Adl26573 Human WSX
4	3498	100.0	2663	2 AAT94120	Aat94120 Alternati
5	3498	100.0	2663	13 ADR25231	Adr25231 Breast ca

6	3498	100.0	2677	4 AAH79286	Aah79286 Cell fact
7	3498	100.0	3258	12 ADL91800	Adl91800 Human PRO
8	3498	100.0	3258	13 ADL14162	Adl14162 Human NF-
9	3494	99.9	2628	6 ABE54548	Abes54548 cDNA enco
10	3494	99.9	2628	8 ACA61018	Acas61018 Human T-c
11	3494	99.9	2628	8 ABX10922	Abx10922 Human int
12	3490	99.8	1911	2 AAC08863	Aac08863 Human DNA
13	3419.5	97.8	2350	8 ACC46162	Acc46162 Human dit
14	3150	90.1	2368	2 AAT94119	Aat94119 Human hae
15	3144.5	89.9	1835	12 ADR20078	Adr20078 Human imm
16	3007	86.0	1760	2 ADO26875	Ado26875 cDNA enco
17	2875	82.2	2213	2 AAZ08867	Aaz08867 Partial h
18	2836.5	81.1	2393	10 ADB36360	Adb36360 Human imm
19	2044	58.4	2005	4 AAS03263	Aas03263 Mouse cdn
20	2044	58.4	2589	2 AAT94121	Aat94121 Mouse hae
21	886.5	25.3	1431	2 AAZ08868	Aaz08868 Partial m
22	405	11.6	817	3 AAA01659	Aaa01659 Human col
23	400	11.4	450	2 AAZ08864	Aaz08864 Mouse DNA
24	381.5	10.9	3400	12 ADK90589	Adk90589 Human IL-
25	381.5	10.9	3400	12 ADM33786	Adm33786 Human IL-
26	381.5	10.9	4040	2 AAT59731	Aat59731 Human int
27	381.5	10.9	4040	3 AAA35207	Aaa35207 Human ade
28	381.5	10.9	4040	3 AAF21329	Aaf21329 Human low
29	381.5	10.9	4040	6 ABK84394	Abk84394 Human cdn
30	381.5	10.9	4040	10 ADE39703	Ade39703 Human int
31	381.5	10.9	4040	10 ADF76394	Adf76394 Novel hum
32	381.5	10.9	4040	10 ABZ97023	Abz97023 Human nuc
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34	381.5	10.9	4040	12 ADOL9579	Adol9579 Human PRO
35	381.5	10.9	4040	13 ADF54648	Adp54648 Human PRO
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37	381.5	10.9	6019	3 AAF21330	Aaf21330 Human low
38	381.5	10.9	6019	10 ABZ97024	Abz97024 Human nuc
39	381.5	10.9	6019	11 ABD20873	Abd20873 Human pul
40	331	9.5	4023	6 ABQ78355	Abq78355 Nucleotid
41	301	8.6	2546	2 AAQ11579	Aaq11579 Encodes g
42	301	8.6	2546	2 AAT47099	Aat47099 Human gra
43	301	8.6	2562	2 AAQ95481	Aaq95481 G-CSFR CD
44	299.5	8.6	2931	2 AAQ11580	Aaq11580 Clone 25-
45	299.5	8.6	2933	2 AAT47100	Aat47100 Human gra

ALIGNMENTS

RESULT 1
AAS03262
ID AAS03262 standard; cDNA; 2646 BP.

AC AAS03262;
DT 07-SEP-2001 (first entry)

DE Human cDNA encoding type I cytokine receptor, hTCCR.

XX Human; type-I cytokine receptor; TCCR; T-cell differentiation; Th1; Th2;
KW agonist; antagonist; autoimmune inflammatory disease;
KW allograft rejection; multiple sclerosis; inflammatory bowel disease;
KW insulin-dependent diabetes mellitus; infectious disease;
KW human immunodeficiency virus; allergic disorder; asthma;
KW allergic rhinitis; HIV; ss.

OS Homo sapiens.

PH Key Location/Qualifiers
CDS 112..2022
FT /*tag= a
FT /product= "hTCCR"
FT sig_peptide 112..218
FT /*tag= b
FT mat_peptide 219..2019
FT /*tag= c
FT /label= Mature_hTCCR
XX

PN WO200129070-A2.
 XX 26-APR-2001.
 XX 18-OCT-2000; 2000WO-US028827.
 PF 20-OCT-1999; 99US-0160542P.
 PR (GETH) GENENTECH INC.
 XX De Sauvage FJ, Grewal I, Gurney AL;
 PI WPI; 2001-308474/32.
 DR P-PSDB; AAU01853.
 DR
 XX Modulating T-cell differentiation and cytokine release profiles into Th1
 PT and Th2 subtypes, for treating immune-related diseases in mammals, by
 PT administering modulator of type I cytokine receptor (TCR).
 XX
 PS Disclosure; Page 122-123; 126pp; English.
 XX
 CC The sequence encodes human type I cytokine receptor, hTCR. The invention
 CC relates to methods of modulating the differentiation of T-cells into the
 CC Th2 subtype instead of the Th1 subtype, by administering a modulator of
 CC TCR (e.g. an antagonist) to enhance, stimulate or potentiate T-cell
 CC differentiation, or using TCR polypeptide or its agonists to prevent,
 CC inhibit or attenuate T-cell differentiation. The mediated disease in
 CC mammal can be treated by administering a TCR antagonist and Th2 diseases
 CC by administering a TCR agonist. Th1-mediated diseases include allograft
 CC rejection and autoimmune inflammatory diseases, such as allergic
 CC encephalomyelitis, multiple sclerosis, insulin-dependent diabetes
 CC mellitus, autoimmune uveoretinitis, inflammatory bowel disease or
 CC autoimmune thyroid disease. Th2-mediated diseases include infectious
 CC diseases, such as leishmania major, Mycobacterium leprae, Candida
 CC albicans, Toxoplasma gondii, respiratory syncytial virus and human
 CC immunodeficiency virus (HIV) and allergic disorders, such as asthma,
 CC allergic rhinitis, dermatitis and vernal conjunctivitis
 XX
 SQ Sequence 2646 BP; 566 A; 779 C; 789 G; 511 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 1.8e-164 Length: 2646
 Score: 3498.00 Matches: 636
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
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 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
 DB 172 CCTCTGTGTGGGTGTCTTTCAGCGGAGCGGTCCCGAGGAGCGCCGGGCGACCTGCG 231
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 DB 232 TGCTACGGAGTTGGACCCCTTGGCGGACTTGAACCTGCTCGTGGGAGCTCTTGGGACCTG 291
 QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
 DB 292 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT 351
 QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 DB 352 GTGGCAGTGGCAGCGGAGCTGGTGGCCATTCTCTGGGAAACAGCTCACCATGCT 411
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
 DB 412 GACAAACTCCTTGTCTGGGGCACTAAGGCGGCGGCGGCTCTCTGGGCGGCGGCTCTTCTG 471

QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
 DB 472 AACCTAGAAACCCAAATGAAGCCAAACGCCCCCGGCTGGGCGCTGAGCGTACTTTTCC 531
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 DB 532 GAGGATGACCCCTCGAGGCGCACTGTCCATTGGGCGCCACCTACATGGCCATCTCATAA 591
 QY 161 ValLeuLysCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 DB 592 GTTCTGTATCTGCAGTCTCCACTACCGAAAGATGTACGAGGCGGCGCTGGACCCCTGTG 651
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluLysGlnAspLeuGluLeuAlaThr 200
 DB 652 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGAGATCCCAAGATTGGAGTACCCACT 711
 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
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 QY 221 SerProLysLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
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 QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280
 DB 892 TGTGTGAGGTGAGCTACAAAGTCTGTTCTGGGTGGAGTGTGAGTGTGAGTCCAGAA 951
 QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
 DB 952 GGAATTACTGTGTGTCTGCTCCCTTAATTCAGTGGGCGGAGTGGGCGGAGTGTCCGCT 1011
 QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
 DB 1012 GTCAAGCCACACAGCTGGAGGCTCTCACCAACCTCTCTTGTGTGTGTGGTTCAGCC 1071
 QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
 DB 1072 TCTGCCCCCGGTAGCGTGGCAGTACAGCAGTGTGGGAGCAGCAGCTACTGTGTGACC 1131
 QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
 DB 1132 TGGCAACCGGGGCGCTGGGGAACCACTGGAGCATGTAGTGGACTGGGCTCGAGTGGGAC 1191
 QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
 DB 1192 CCCCTGGAGAAACTCACTACCTGGGTCCGGCTTCCCCCTGGGAACCTCAGTGTCTGTACCA 1251
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 DB 1432 CCAAGGCCACGAGTTCGAGGCGCACCTCACCCACTACACTTGTGTGTGCACAGAGTGGAAAC 1491
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 1552 CTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT 1611
 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
 1612 GGTCCCATCTCCGGCTTCATCTACCAAGATACACCTGAGTGGAAAGTTCTGCCGGC 1671
 521 IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
 1672 ATCCTATTCTTGTGGGGTGTTCCTGTGTGGGGTGTGGCCTGAGCCTGGCCACCTCTGGA 1731
 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
 1732 AGTGTCTACCACTTAAGGCACAAAGTGTGCCCCGCTGGGTCTGGGAGAAAGTTCTCTGAT 1791
 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
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 1912 CAGCCCCCAGGCCAGCCGCCCTTGTGACTCTGGGTATGAGAGACATCTCTGCCACACA 1971
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 1972 CTTGAGGAGCTGGGCCCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2019
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 ID ADD68150 standard; cDNA; 2657 BP.
 AC ADD68150;
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 DT 15-JAN-2004 (first entry)
 XX
 DE Human WSX-1 receptor cDNA SEQ ID NO:8.
 XX
 KW ss; gene; human; zcytor17; antiinflammatory; dermatological;
 KW immunosuppressive; antimicrobial; vaccine; inflammatory disease;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
 KW toxic shock syndrome; infectious disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 133..2043
 FT /*tag= a
 FT /product= "WSX-1 receptor"
 XX
 PN WO2003060090-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 21-JAN-2003; 2003WO-US001984.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 25-APR-2002; 2002US-0375323P.
 PR 19-DEC-2002; 2002US-0435315P.
 PR
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprechter CA, Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;
 PI Novak JE, Gross JA, Dillon SR;
 XX
 DR WPI; 2003-618179/58.
 DR P-PSDB; ADD68151.
 XX

PT New zcytor17 ligand polypeptides, useful for treating inflammatory
 PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
 PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.
 XX
 PS Example 3; SEQ ID NO 8; 372pp; English.
 XX
 CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
 CC polypeptide of the invention has antiinflammatory, dermatological,
 CC immunosuppressive, and antimicrobial activity, and may have a use in a
 CC vaccine. The polypeptide is useful for treating inflammatory diseases,
 CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
 CC shock syndrome or infectious diseases. The present sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 2657 BP; 556 A; 789 C; 800 G; 512 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.8e-164 Length: 2657
 Score: 3498.00 Matches: 636
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
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 DB 133 ATCGGGGAGGAGGGGGCCCTTCTTGGCTGTGGCCGCTGCCAAGCTGGCGCTGCTG 192
 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
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 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 DB 253 TGCTACGAGTTGGACCCCTTGGGCGACTTGAACCTGCTCGGGAGCGCTCTTGGGAGCTG 312
 QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
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 QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
 DB 493 AACCTAGAAACCCAAATGAAGCCAAACGCCCGCTGGGCGCTGACGTGGAGCTTTTCC 552
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 DB 553 GAGGATGACCCCTCGGAGGCGCACTGTCCATTGGGCCCCACCTACATGCCCATCTCATAAA 612
 QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaThrThrLeuLeuGlu 180
 DB 613 GTTCTGATCTGCCAGTTTCCACTACCGAAGATGTTCAGGAGCGCGCTGGACCCCTGCGAA 672
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
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 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
 DB 733 GGCTACAAAGTGTATGGCGCTGCCGATGAGAGAAAGAGAGGATTTGTGGGCGAGTGG 792
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 Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
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 Db 1993 CCTGAGGAGCTGGGCTTCTGGGGCCCCCAGCCACAGGTTCTGGCC 2040
 RESULT 3
 ADL26573
 ID ADL26573 standard; DNA; 2657 BP.
 XX
 AC ADL26573;
 XX 20-MAY-2004 (first entry)
 XX Human WSX-1 receptor DNA.
 XX antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; haematopoietic cell;
 KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
 KW haematopoietic progenitor cell; zcytor17lig-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KW septicemia; toxic shock syndrome; zcytor17lig; human; gene; ds;
 KW zcytor17 ligand; WSX-1 receptor.
 XX Homo sapiens.
 OS
 XX US2003215938-A1.
 PN
 XX 20-NOV-2003.
 PD
 XX 21-JAN-2003; 2003US-00351157.
 PF
 XX 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 PI P-PSDB; ADL26574.
 DR WPI; 2003-876545/81.
 DR P-PSDB; ADL26574.
 XX Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 XX Example 3; SEQ ID NO 8; 205pp; English.
 PS
 XX The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC sequence, given in specification, or at least one polypeptide

comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (C1) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for: reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor17lig-induced proliferation or differentiation of hematopoietic cells and hematopoietic progenitor cells; reducing zcytor17lig-induced inflammation; treating a mammal afflicted with an inflammatory disease in which zcytor17lig plays a role. The disease is a chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and psoriasis. The disease is acute inflammatory disease such as endotoxaemia, septicaemia, toxic shock syndrome and infectious disease. An immune response inhibiting composition is useful for inhibiting an immune response in a mammal exposed to an antigen or pathogen. An inflammatory response inhibiting composition is useful for suppressing an inflammatory response in a mammal with inflammation. An antibody that specifically binds to (I) is useful for detecting the presence of a multimeric or heterodimeric cytokine receptor in a biological sample. CC This sequence encodes a human WSX-1 receptor used in the creation of a CC vector expressing full length zcytor17.

XX
SQ Sequence 2657 BP; 556 A; 789 C; 800 G; 512 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.8e-164 Length: 2657
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-088-950A-1 (1-636) x ADL26573 (1-2657)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 133 ATGGGGGAGCGAGGGGGCCCCCTTCTGGGTGGGGCGCTGGCCCAAGCTGGGGCGCTCTG 192
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 193 CCTCTGTGTGGGTGCTTTTCCAGCGGACGGCTCCCGAGGGCAGCGCGGGCCACTGCAG 252
Qy 41 CysTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 253 TGCTACGAGTTGACCTTGGGCGACTTGAACCTGCTCGTGGGAGCCCTCTTGGGACCTG 312
Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTrpArgSerAsnLysThrGlnThr 80
Db 313 GAGGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT 372
Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
Db 373 GTGGCAGTGGCAGCGGAGCGAGCTGGGTGGCCATTCTCTGGGNAACAGCTCACCATGTCT 432
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120
Db 433 GACAAATCTTGTCTGGGCACTAAGCGAGGCGAGCCCTCTCTGGCCCCCGCTTTCGTG 492
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db 493 AACCTAGAAACCCCAATGAAAGCCAAACGCCCGGCTGGGCGCTGACGTGGACTTTTTC 552
Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
Db 553 GAGATGACCCCTGGAGGCGACTGTCCATTGGGCCCCACCTACATGGCCATCTCATAAA 612
Qy 161 ValLeuIleCysGlnPheHisTrpArgArgCysGlnGluAlaIleTrpThrLeuLeuGlu 180
Db 613 GTTCTGATCTGCCAGTTCCTACCTACCGAAGATGTCCAGGAGGGCGCTGACCCCTCTGAA 672
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
Db 673 CCGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAGATTTGGAGCTAGCCACT 732

Qy 201 GlyTrpLysValTrpGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
Db 733 GGCTACAAAGTGTATGCCCGCTGCCGATGCAGAAAGAGAGGATTTGTGGGCGAGTGG 792
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
Db 793 AGCCCCATTTTGTCTTCCAGACACCGCTTCTGCTCCAAAGATGTGTGGGTATCAGGG 852
Qy 241 AsnLeuCysGlyThrProGlyGlyGluProLeuLeuLeuTrpLysAlaProGlyPro 260
Db 853 AACCTCTGTGGGAGCGCTGGAGAGAGAACTTTGCTTCTATGGAAGGCCCCAGGGGCC 912
Qy 261 CysValGlnValSerTrpLysValTrpPheTrpValGlyArgGlyLeuSerProGlu 280
Db 913 TGTGTGCAGGTGAGCTACAAAGTCTGCTTCTGGGTTGGAGGTCTGTGAGTCCAGAA 972
Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
Db 973 GGAATTACCTGCTGCTCCCTAAATCCAGTGGGCGGAGTGGGCGAGGTCTCCGCT 1032
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
Db 1033 GTCAACGCCCAAGCTGGGAGCGCTCTCAACCACTCTCTTTGGTCTCTTGGATTACGCC 1092
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
Db 1093 TCTGCCCGCCGTCAGTGGCGAGTCAGCAGCATCGCTGGGAGCAGGAGCTACTGTCGCC 1152
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
Db 1153 TGGCAACCGGGGCTCGGGGAACCACTGGAGCATGTAGTACCTGGGCTCGAGATGGGGAC 1212
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
Db 1213 CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCGCTGGGAACCTCAGTGTCTGTATTACA 1272
Qy 381 GlyAsnPheThrValGlyValProTrpArgIleThrValThrAlaValSerAlaSerGly 400
Db 1273 GGGAAATTCATCTGTGGGTCCCTTCATCGAATCACTGTGACCGCAGTCTCTGCTTCAGC 1332
Qy 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluLeuAlaProLeuValGlyPro 420
Db 1333 TTGGCCTCTGCATCTCCGCTCTGGGGTTCAGGGAGAAATTAGCACCCCTAGTGGGGCCA 1392
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db 1393 ACCTTTGGGACTCCAAAGATGCCCTCCAGGGAGCCCCCGCCATAGCGTGGGAGAGGTC 1452
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTrpThrLeuCysAlaGlnSerGlyThr 460
Db 1453 CCAAGGCACCACTTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGGAAACC 1512
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1513 AGCCCCCTCGTCTGCATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT 1572
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1573 CCTTGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT 1632
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1633 GGTCCCATCTCCGGCTTCATCTACAGATACACCTCAGGTGGAAAGTCTTCCGACGCC 1692
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1693 ATCCTATTCTTGGGGCTTGTCTCTGTTGGGGTGTGGCTGAGCTGAGCTGGCCACTCTCGA 1752
Qy 541 ArgCysTrpHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1753 AGGTGCTACCACTAAGGCACAAAGTGTGCCCCCTGGGTCTGGGAGAAAGTTCCTGAT 1812

QY 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
 Db 1813 CTTGCCAACAGCAGTTTCAGGCCAGCCACATGAGCAAGTACCTGAGGCCAGCCCTT 1872
 QY 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600
 Db 1873 GGGGACTTCCCATCTCGAAGTGGAGGAGATGGAGCCCGCCCGGTTATGAGTCCCTCC 1932
 QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
 Db 1933 CAGCCCGCCAGCCACCCCGCTTGACTCTGGGTATGAGAGCATTCTGCGCCACA 1992
 QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
 Db 1993 CCTGAGGAGCTGGGCTTCTGGGGCCCCCGCCAGCCACAGGTTCTGGCC 2040
 RESULT 4
 AAT94120
 ID AAT94120 standard; cDNA; 2663 BP.
 AC AAT94120;
 XX
 DT 22-MAY-1998 (first entry)
 DE Alternatively spliced Zcytor1 cDNA.
 KW Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;
 KW cancer diagnosis; agonist; antagonist; alternatively spliced; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 139..2049
 FT /*tag= a
 FT /product= "Zcytor1"
 XX
 PN WO9744455-A1.
 XX
 PD 27-NOV-1997.
 XX
 PF 19-MAY-1997; 97WO-US008502.
 XX
 PR 23-MAY-1996; 96US-00653740.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Baugartner JW, Foster DC, Grant FJ, Sprecher CA;
 XX
 DR WPI; 1998-018509/02.
 DR P-PSDB; AAW33399.
 XX
 PT Haematopoietic cytokine receptor - useful for ligand detection, and
 PT pathological condition diagnosis.
 XX
 PS Claim 13; Page 46-51; 86pp; English.
 XX
 CC The present sequence encodes an alternatively spliced human
 CC haematopoietic cytokine receptor Zcytor1, useful for ligand detection,
 CC and pathological condition diagnosis, including cancer. Receptor agonists
 CC of the protein can be used to stimulate the proliferation and development
 CC of target cells in vitro and in vivo. The agonists can stimulate cell
 CC mediated immunity and lymphocyte proliferation, to treat infection
 CC involving immunosuppression, e.g. viral infections. They may also be used
 CC to suppress tumours, induce cytotoxicity, treat leukopaenias and enhance
 CC the regeneration of the T-cell repertoire after bone marrow
 CC transplantation. Antagonists of the protein may be used to suppress the
 CC immune system, treat autoimmune diseases, including rheumatoid arthritis,
 CC multiple sclerosis and diabetes mellitus. Immune suppression caused by
 CC the antagonists can also be used to reduce rejection of tissue or organ
 CC transplants and grafts, and to treat T-cell specific leukaemias and
 CC lymphomas
 XX
 SQ Sequence 2663 BP; 558 A; 790 C; 803 G; 512 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,81e-164 Length: 2663
 Score: 3498.00 Matches: 636
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-088-950A-1 (1-636) x AAT94120 (1-2663)
 QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
 Db 139 ATCGGGGAGGAGGGGGCGCCCTTTCTGGGTGTGGCGCTGCCCAAGTGGCGGTGTG 198
 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
 Db 199 CCTCTGTGTGGGTGCTTTTCCAGCGGACGGCTCCCGAGGCGAGCGCGGCCACTGAG 258
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 Db 259 TGCTACGGAGTTGGACCTTGGCGGACTTGAACGTCTGTGGGAGCCTCTTGGGACCTG 318
 QY 61 GlyAlaProSerGluLeuHisGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
 Db 319 GGAGCCCTCTCCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCAAACAAACCCAGACT 378
 QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 Db 379 GTGGCAGTGGGAGCGGAGCGGAGCTGGGTGGCCATTCTCCGGAACAGACTACCATGCT 438
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
 Db 439 GACAACTCTTGTCTGGGGCACAATAAGGCAGGCCAGCCTCTCTGGCCCCCGCTCTTCGTG 498
 QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
 Db 499 AACCTAGAAACCCAAATGAAGCCAAACGCCCGCGCTGGGCGCTGAGCTGGACTTTTCC 558
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 Db 559 GAGGATGACCCCTCTGGAGGCCACTGTCTCATTTGGGGCCCCACCTACATGGCCATCTCATATA 618
 QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 Db 619 GTTCTGATCTGCCAGTTCCACTTACCGAAGATGTCCAGGAGCGGCGCTGGACCTGTGGAA 678
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
 Db 679 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAGATTTGGAGTAGCCACT 738
 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAlaAspLeuTrpGlyGluTrp 220
 Db 739 GGCTACAAAGTGTATGGCCGCTGCGCGATGGAGAAGAAGAGGATTTGGGGCGGAGTGG 798
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
 Db 799 AGCCCCATTTGCTCTTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 858
 QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
 Db 859 AACCTCTGTGGGACCCCTGGAGGAGGAACCTTTGTCTTATGGAAGCCCGCCAGGGCCC 918
 QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280
 Db 919 TGTGTGAGGTGAGCTACAAAGTCTGGGTGGAGGTCTGTGAGCTGAGTCCAGAA 978
 QY 281 GlyIleThrCysCysSerSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
 Db 979 GGAATTACTGTCTGCTCTCCCTAATTCCAGTGGGGCGGAGTGGGCCAGGGGTGTCCGCT 1038
 QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320

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Db 1039 GTCACGCCACAGCTGGAGCCTCTCACCAACCTCTCTTGGTCTGCTGGATTCAGCC 1098
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
Db 1099 TCTGCCCTCCGTCAGCTGGAGTCCAGCAGCATCGCTGGAGCAGGAGCTACTGGTACC 1158
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
Db 1159 TGGCAACCGGGGCTGGGAACCACTGGAGCATGTAGTGGAGTGGGCTCGAGATGGGGAC 1218
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyValAsnLeuSerAlaLeuPro 380
Db 1219 CCCCTGGAGAACTCAACTGGTCCGGCTTCCCTCGGAACCTCAGTCTCTGTATACCA 1278
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db 1279 GGGAAATTCAGTGTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1338
Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1339 TTGGCCTCTGCATCTCCGCTTGGGGGTTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA 1398
Qy 421 ThrLeuTrpArgLeuGlnAsnAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db 1399 ACGTTTGGGACATCCCAAGATGCCCTCCAGGGACCCCGCCATAGCGTGGGGAGAGGTC 1458
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db 1459 CCAAGGCACAGCTTCAGGCCACCTCACCACTACCTGTGTGTGCACAGAGTGGNACC 1518
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1519 AGCCCTCCCTCTGCATGAATGTGAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT 1578
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1579 CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGTGGACAGGGCCCTCCT 1638
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1639 GGTCCCATCTCCGGCTTCATCTACCAAGATACACCCCTGAGGTGGAAAGTTCTGCCAGGC 1698
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1699 ATCTATTCTTGTGGGCTTGTTCCTGTGGGGTGTGGCTGAGCCTGGCCACCTCTGGA 1758
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1759 AGGTGCTTACCCTAGGCCACAAAGTGTCTCCCGCTGGGTCTGGGAGAAAGTTCTCTGAT 1818
Qy 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1819 CTGTCCCAAGCAGATTTCAGGCCAGCCCCACATGAGCAAGTACTGTAGGGCCCGAGCCCTT 1878
Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600
Db 1879 GGGGACTTGCCTCTCTGGAAGTGGAGAGATGAGAGCCCGCGCGTATATGAGATCTCTCC 1938
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1939 CAGCCCGCCAGGCCACCGCCCGCTTGTACTCTGGGTATGAGAAGCACATTCCTCTGCCACA 1998
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1999 CCTGAGGAGCTGGGCTTCTTGGGGCCCCCGCCAGGCCACAGGTTCTTGGCC 2046
```

RESULT 5

ADR25231

ID ADR25231 standard; DNA; 2663 BP.

XX AC

XX ADR25231;

XX DT

21-OCT-2004 (first entry)

```
XX Breast cancer prognosis marker #1092.
DE de; breast cancer; prognosis; gene expression; diagnosis.
KW Homo sapiens.
OS WO2004065545-A2.
PN 05-AUG-2004.
PD 15-JAN-2004; 2004WO-US001100.
PX 15-JAN-2003; 2003US-00342887.
PR (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX Van't Veer LJ, He Y;
PI WPI; 2004-593473/57.
XX
XX Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
XX Disclosure; SEQ ID NO 1092; 226pp; English.
XX
XX The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
XX Sequence 2663 BP; 558 A; 790 C; 803 G; 512 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.81e-164 Length: 2663
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-088-950A-1 (1-636) x ADR25231 (1-2663)
Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 139 ATGCGGGAGGAGGAGGGGCGCCCTTTCTGGCTGTGGCCGCTGCCAAGCTGGCGCTGCTG 198
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 199 CCTCTGTGTGGGTGCTTTTCCAGCGGACGCGTCCCAGGGCAGCGCCGGCCACTGCAG 258
Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 259 TGCTACGGAGTTGGACCCCTTGGCGCACTTGAACCTGCTGTGGGAGCCTCTTGGGAGCCTG 318
Qy 61 GlyAlaProSerGluLeuHisIleuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
Db 319 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCCAACAAACCCAGACT 378
Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
Db 379 GTGGCAGTGGCAGCCGAGCGAGCTGGTGGCCATTCTCTCGGAAACAGCTCACCATGTCT 438
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
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Sequence 2677 BP; 581 A; 786 C; 798 G; 512 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.82e-164 Length: 2677
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-088-950A-1 (1-636) x AAH79286 (1-2677)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 126 ATGCGGGGAGCAGGGGGGCGCCCTTTCTGGCTGTGGCGCTGCCCAAGCTGGCGCTGCTG 185
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 186 CCTCTGTGTGGGTGCTTTTCCAGCGACGCGCTCCCGAGGCGAGCGCGGCGCACTGCAG 245
Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 246 TGCTACGGAGTGGACCTTGGGCGACTTGNACTGCTGTGGGAGCCCTCTTGGGACCTG 305
Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
Db 306 GGAGCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT 365
Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
Db 366 GTGCACTGGCGAGCGCGAGCGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGTCT 425
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
Db 426 GACAACTCTTGTCTGGGCGACTAGGCGAGCGCGAGCTCTTGGCCCGCCGCTTCGTG 485
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db 486 AACCTAGAAACCCAAATGAAGCCAAACGCCCCCGGCTGGGCGCTGACGTGGACTTTTCC 545
Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
Db 546 GAGGATACCCCTCGGAGGCGACTGTCTCATTTGGGCGCCACCTACATGCCCATCTCTATAA 605
Qy 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
Db 606 GTTCTGATCTGCCAGTTCCACTACCGAAGATGTCCAGAGGCGGCGCTGGACCTCTGGAA 665
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
Db 666 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAAAGATTGGAGCTAGCCACT 725
Qy 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
Db 726 GGTGTACAAAGTGTATGCGCGCTGCGGATGAGAAAGAGGATTTGTGGGCGAGTGG 785
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
Db 786 AGCCCCATTTGTCTTCCAGACACCGCCCTCTGCTCCAAAGATGTGGGTATCAGG 845
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
Db 846 AACCTCTGTGGAGCGCTCGGAGGAGGAGAACCTTTGTTCTATGGAAGGCCCGGAGGCC 905
Qy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280
Db 906 TGTGTGAGGTGAGTACAAAGTCTGGTCTTGGGTCTGGAGTCTGTGAGTCTGAGTCCAGAA 965
Qy 281 GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
Db 966 GGAATTAACCTGCTGCTCTCCCTAAATCCAGTGGGCGGAGTGGGCGAGGCTCCGCT 1025
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320

RESULT 7

ADL91800

ID ADL91800 standard; cDNA; 3258 BP.

XX

AC ADL91800;

XX

Db 1026 GTCAAGCCACAAAGCTGGGAGCCTCTCACCACCTCTCTTTGGTCTCTCTGGATTACGCC 1085
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
Db 1086 TCTGCCCCCGTACGCTGGGAGTGCAGCAGCATGCTGGGAGCAGGAGCTACTGTGACCC 1145
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
Db 1146 TGGCAACCGGGGCTGGGAAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1205
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
Db 1206 CCCCTGGAGAAATCAACTGGGTCCGGCTCCCGCTGGGAACCTCAGTGTCTCTTACCA 1265
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db 1266 GGGAAATTTCACTGTGGGGTCCCGCTATCGAATCACTGTGACCGCAGTCTCTGTCTCAGGC 1325
Qy 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1326 TTGGCCTCTGCATCCTCCGCTCTGGGGTTCAGGGAGGAATTAGCACCCCTAGTGGGCGCA 1385
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db 1386 ACGTTTGGCGACTCCAAAGATGCCCTCCAGGGACCCCGCCCATAGCGTGGGAGAGGTC 1445
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db 1446 CCAAGGCACCAAGTTCAGGCGCCACCTCACCACTTACACCTTGTGTGCACAGAGTGAACC 1505
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1506 AGCCCTCCGCTCTGCATGATGTAGTGGGCAACACACAGAGTGTACCCCTGCCTGACCTT 1565
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1566 CCTTGGGTCCCTGTGAGCTGTGGTGCACAGCATCTACCATCGCTGGACAGGCGCTCCT 1625
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1626 GGTCCCATCCTCCGGCTTCACTACCAAGATAACACCCCTGAGGTGGAAGTTCTGCCGGGC 1685
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1686 ATCTATTCTTGTGGGCTTGTCTTGTGGGTGTGGCTGAGCCTGGCCACCTCTGGA 1745
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1746 AGGTGCTTACCACCTAAGGCACAAAGTGTGCCCGCTGGGTCTGGGAGAAAGTTCTCTGAT 1805
Qy 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1806 CCTGCCAACAGCATTTAGGCCAGCCCCACATGAGCAAGTACCTTAGGGCCAGCCCTT 1865
Qy 581 GlyAspLeuProIleLeuGluValGluMetGluProProProValMetGluSerSer 600
Db 1866 GGGGACTTGGCCATCTTGAAGTGGAGAGATGAGCCCCCGCGGTATTGGAGTCTCTCC 1925
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1926 CAGCCCCCGGAGCCACCGCCCGCTTGTACTCTGGGTATGAGAAGCACTTCTCTGCCACCA 1985
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1986 CCTGAGAGCTGGGCGCTTCTGGGGCGCCCCCAGGCCACAGGTTCTTGCC 2033

DT	17-JUN-2004 (first entry)	CC	polyneuropathy, Guillain-Barr syndrome, chronic inflammatory
XX		CC	demyelinating polyneuropathy, hepatobiliary disease, infectious or
DE	Human PRO34336 encoding cDNA SEQ ID NO:21.	CC	autoimmune chronic active hepatitis, primary biliary cirrhosis,
XX		CC	granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
KW	human; PRO; immune related disease; immunosuppressive; dermatological;	CC	disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or
KW	hepatotropic; nephrotropic; antidiabetic; antiaesthetic; antipsoriatic;	CC	immune-mediated skin disease, bullous skin disease, erythema multiforme,
KW	antiallergic; antianemic; antiarteriosclerotic; antiarthritic;	CC	contact dermatitis, psoriasis, allergic disease, asthma, allergic
KW	neuroprotective; respiratory; antiinflammatory; gene therapy;	CC	rhinitis, atopic dermatitis, food hypersensitivity, urticaria,
KW	immune related disorder; systemic lupus erythematosus;	CC	immunologic disease of the lung, eosinophilic pneumonia, idiopathic
KW	rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;	CC	pulmonary fibrosis, hypersensitivity pneumonitis, transplantation
KW	spondyloarthropathy; systemic sclerosis;	CC	associated disease, graft rejection or graft-versus-host-disease. The
KW	idiopathic inflammatory myopathy; Sjogren's syndrome;	CC	present sequence encodes a novel human PRO protein from the present
KW	systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;	CC	invention.
KW	autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;	XX	Sequence 3258 BP; 722 A; 942 C; 964 G; 630 T; 0 U; 0 Other;
KW	immune-mediated renal disease; demyelinating disease;	SQ	
KW	idiopathic demyelinating polyneuropathy; Guillain-Barr syndrome;		
KW	chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;		
KW	infectious hepatitis; autoimmune chronic active hepatitis;		
KW	primary biliary cirrhosis; granulomatous hepatitis;		
KW	sclerosing cholangitis; inflammatory bowel disease;		
KW	gluten-sensitive enteropathy; Whipple's disease;		
KW	immune-mediated skin disease; bullous skin disease; erythema multiforme;		
KW	contact dermatitis; psoriasis; allergic disease; asthma;		
KW	allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria;		
KW	immunologic disease; eosinophilic pneumonia;		
KW	idiopathic pulmonary fibrosis; hypersensitivity pneumonitis;		
KW	transplantation associated disease; graft rejection;		
KW	graft-versus-host-disease; gene; ss.		
XX	Homo sapiens.		
OS			
XX			
PH	Key		
FT	Location/Qualifiers		
FT	424..2334		
FT	/tag= a		
FT	/product= "PRO34336"		
XX	WO2004024076-A2.		
PN			
XX			
PD	25-MAR-2004.		
XX			
PF	10-SEP-2003; 2003WO-US028361.		
XX			
PR	11-SEP-2002; 2002US-0410174P.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;		
PI	Williams PM, Wood WI, Wu TD;		
XX			
DR	WPI: 2004-269874/25.		
DR	P-PSDB; ADL91801.		
XX			
PT	New PRO nucleic acid useful for preparing a composition for diagnosing or		
PT	treating an immune related disorder, e.g., systemic lupus erythematosus		
PT	in a mammal.		
XX			
PS	Claim 2; SEQ ID NO 21; 200pp; English.		
XX			
CC	The present invention describes isolated nucleic acid sequences encoding		
CC	novel proteins (PRO), which can be used in the treatment of immune		
CC	related diseases. The PRO sequences have immunosuppressive,		
CC	dermatological, hepatotropic, nephrotropic, antidiabetic, antiaesthetic,		
CC	antipsoriatic, antiallergic, antianemic, antiarteriosclerotic,		
CC	antiarthritic, neuroprotective, respiratory and antiinflammatory		
CC	activities, and can be used in gene therapy. The PRO nucleic acids or		
CC	proteins can be used for preparing a composition for diagnosing or		
CC	treating an immune related disorder, e.g., systemic lupus erythematosus,		
CC	rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,		
CC	spondyloarthropathy, systemic sclerosis, idiopathic inflammatory		
CC	myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,		
CC	autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis,		
CC	diabetes mellitus, immune-mediated renal disease, a demyelinating disease		
CC	of the central or peripheral nervous system, idiopathic demyelinating		

CC	polyneuropathy, Guillain-Barr syndrome, chronic inflammatory		
CC	demyelinating polyneuropathy, hepatobiliary disease, infectious or		
CC	autoimmune chronic active hepatitis, primary biliary cirrhosis,		
CC	granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel		
CC	disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or		
CC	immune-mediated skin disease, bullous skin disease, erythema multiforme,		
CC	contact dermatitis, psoriasis, allergic disease, asthma, allergic		
CC	rhinitis, atopic dermatitis, food hypersensitivity, urticaria,		
CC	immunologic disease of the lung, eosinophilic pneumonia, idiopathic		
CC	pulmonary fibrosis, hypersensitivity pneumonitis, transplantation		
CC	associated disease, graft rejection or graft-versus-host-disease. The		
CC	present sequence encodes a novel human PRO protein from the present		
CC	invention.		
XX	Sequence 3258 BP; 722 A; 942 C; 964 G; 630 T; 0 U; 0 Other;		
SQ			
	Alignment Scores:		
	Pred. No.:	2.23e-164	Length: 3258
	Score:	3498.00	Matches: 636
	Percent Similarity:	100.00%	Conservative: 0
	Best Local Similarity:	100.00%	Mismatches: 0
	Query Match:	100.00%	Indels: 0
	DB:	12	Gaps: 0
	US-10-088-950A-1 (1-636) x ADL91800 (1-3258)		
QY	1 MetArgGlyValArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20		
DB	424 ATGCGGGAGGAGCGGGCGCCCTTTCTGGTGTGGCGCTGCCCAAGCTGGCGGTG 483		
QY	21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40		
DB	484 CCTCTGTTGGTGCTTTTCCAGCGGACGGCTCCCGAGGGCAGCGCGGCACATGAG 543		
QY	41 CysTyrGlyValGlyProLeuGlyAspLeuAenCysSerTrpGluProLeuGlyAspLeu 60		
DB	544 TGCTACGGAGTTGGACCTTGGCGACTTGAACGTCTCGTGGAGCCTTTGGGACCTG 603		
QY	61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80		
DB	604 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAAGTACCCTGCCAACAACCAGACT 663		
QY	81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100		
DB	664 GTGGCAGTGGCAGCGGAGGAGCTGGTGGCCATCTCTGGGAACAGCTACCATGTCT 723		
QY	101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120		
DB	724 GACAAACTCTTGTCTGGGGCACTAAGGACAGCCAGCCCTCTCTGGCCCCCTCTCGTG 783		
QY	121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140		
DB	784 AACCTAGAAACCAATGAAGCCAAACCCCCCGCTGGGGCCCTGAGCTGACTTTTCC 843		
QY	141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160		
DB	844 GAGGATGACCCCTGGAGGCCACTGTCCATTGGGGCCCACTACATGSCCATCTCATAA 903		
QY	161 ValLeuLysCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180		
DB	904 GTTCTGATCTGCAGTTCACCTACCGAAGATGTCCAGGAGGGCGCTGGACCTGTGGAA 963		
QY	181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200		
DB	964 CCGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCCAAGATTTGAGTACCCACT 1023		
QY	201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220		
DB	1024 GCCTACAAAGTGTATGGCGCTGCCGGATGGAGAAGAGAGGATTTGTGGGGCCAGTG 1083		
QY	221 SerProLysLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240		
DB	1084 AGCCCCATTTTGTCTTCCAGACACCGCCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 1143		

Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260.
Db 1144 AACCTCTGTGGAGCGCTGGAGGAGAGAACTTTGCTTCTATGGAAGGCCCGCCAGGCGCC 1203
Qy 261 CysValGlnValSerThrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
Db 1204 TGTGTGAGGTGAGCTACAAAGTCTGGTTCCTGGGTTCGAGTCTGAGCTGAGTCCAGAA 1263
Qy 281 GlyThrCysCysCysSerLeuLeuProSerGlyAlaGluTrpAlaArgValSerAla 300
Db 1264 GGAATTACCTGCTGCTCTCCCTAAATCCAGTGGGGGGAGTGGCCAGGGTGTCCGCT 1323
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
Db 1324 GTCAACGCCCAAGCTGGAGCTCTCACCACCTCTCTTTGGTCTGCTTGGATTACGCC 1383
Qy 321 SerAlaProArgSerValAlaValSerSerLeuAlaGlySerThrGluLeuValThr 340
Db 1384 TCTGCCCCCGTAGCGTGGCAGTCAGCAGCATCGCTGGGAGCAGGAGCTACTGTGTGACC 1443
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
Db 1444 TGGCAACCGGGCTGGGGAACCACTGGAGCATGTAGTGGCTCGAGATGGGGAC 1503
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
Db 1504 CCCCTGGAGAACTCAACTGGTCCGGCTCCCGCTGGGAACCTCAGTGTCTGTACCA 1563
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db 1564 GGGAAATTCATGTCGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGTCTCAGGC 1623
Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1624 TTGGCTCTGCATCTCGTCTGGGGTTGAGGAGGAATTAGCACCCCTAGTGGGGCCA 1683
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db 1684 ACGCTTTGGCGACTCCAAAGATGCCCTCCAGGAGCCCGCCCATAGCTGGGGAGAGTTC 1743
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db 1744 CCAAGGCACCACTTCAGAGCCACCTCACCACCTACACCTGTGTGACACAGAGTGGAAAC 1803
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1804 AGCCCTCCGCTGTCATGATGTGAGTGGAACACACAGAGTGTACCCCTGCCTGACCTT 1863
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1864 CCTTGGGTCCCTGTGAGCTGTGGTGACAGCATCTACCATCGTGACAGGGCCCTCCT 1923
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1924 GGTCCCATCTCCGGCTTCATCTACCAAGATAACACCTGAGTGGAAAGTTCTGCCGGGC 1983
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1984 ATCTATCTTGTGGGGCTGTGTCCTGTGGGTGGCTGAGCTGGCCACCTCTGGA 2043
Qy 541 ArgCysThrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 2044 AGGTGCTACCACTAAGGCACAAAGTGTCTCCCGCTGGTCTGGGAGAAAGTTCTTGAT 2103
Qy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 2104 CCTGCCAACAGCATTCAGGCCACGCCCCACATGAGCAAGTACCTGAGGGCCAGCCCTT 2163
Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600
Db 2164 GGGGACTTGGCCATCTCGGAAGTGGAGGATGAGGCCCGCGGGTATGGAGTCTCTCC 2223

Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 2224 CAGCCGCCCGCCAGGCCACCGCCGCTTACTCTGGGTATGAGAAGCACTTCTCTGCCACA 2283
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 2284 CTTGAGAGCTGGGCTTCTGGGGCCCCCGCCAGGCCACAGGTTCTGGCC 2331
RESULT 8
ADRI14162
ID ADR14162 standard; DNA; 3258 BP.
XX
AC ADR14162;
XX
XX 21-OCT-2004 (first entry)
XX
DE Human NF-kappaB pathway-associated gene SeqID163.
XX
KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnery; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; hepatitis B; hepatitis C; BSV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; gene; ds; human.
XX
OS Homo sapiens.
XX
PN WO2004065577-A2.
XX
PD 05-AUG-2004.
XX
XX 13-JAN-2004; 2004WO-US000798.
PF
XX 14-JAN-2003; 2003US-0440068P.
PR
XX 12-MAY-2003; 2003US-0469757P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Nadler SG, Neubauer MG, Feder JN, Carman J;
XX
XX WPI; 2004-562168/54.
DR P-PSDB; ADR14163.
XX
XX New isolated polynucleotides and polypeptides associated with NF-kappaB
PT pathway, useful for diagnosing, treating, or preventing disorders or
PT diseases associated with NF-kappaB pathway.
XX
PS Claim 1; SEQ ID NO 163; 237pp; English.
XX
CC This invention relates to the novel association of protein sequences (and
CC the genes which encode them) to the NF-kappaB pathway. The invention may
CC be useful for the production of compounds with an antiinflammatory,
CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
CC vulnery activity or for gene therapy. The proteins and nucleotides are
CC useful for diagnosing, preventing, treating, or ameliorating conditions
CC or diseases associated with the NF-kappaB pathway. The condition is an
CC immune disorder, an inflammatory disorder, an inflammatory disorder
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human gene which is
 CC subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 SQ Sequence 3258 BP; 722 A; 942 C; 964 G; 630 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,23e-164 Length: 3258
 Score: 3498.00 Matches: 636
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DE: 13 Gaps: 0

US-10-088-950A-1 (1-636) x ADR14162 (1-3258)

QY 1 MetArgGlyValArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
 DB 424 ATGCGGGAGGAGGCGGCGCCCTTTCTGGCTGTGGCGCGCTGCCAAGCTGGCGTGTG 483
 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
 DB 484 CCTCTGTTGGTGTCTTTTCAGCGGAGCGCTCCCGAGGAGCGCGCGGCGACCTGCGAG 543
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAenCysSerTrpGluProLeuGlyAspLeu 60
 DB 544 TGCTACGGAGTTGGACCTTGGCGGACTTGAATGCTGCTGGGAGCGCTCTTGGGACCTG 603
 QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
 DB 604 GGAGCCCCCTCCGAGTTACCTCTCAGAGCCAAAGTACCTGTCCAAACAAACCCAGACT 663
 QY 81 ValAlaValAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 DB 664 GTGGAGTGGCAGCGGAGCTGGTGGCCATCTCTCGGGAACAGCTCACCATGCT 723
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
 DB 724 GACAAACTCCTGTCTGGGGCACTAAGGCAGGCGGCGGCTCTGGGCCCCCGCTTCTG 783
 QY 121 AenLeuGluThrGlnMetLysProAenAlaProArgLeuGlyProAspValAspPheSer 140
 DB 784 AACCTAGAAACCCAAATGAAGCCAAACGCGCCCGGCTGGGCGCTGACGTGACTTTTCC 843
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 DB 844 GAGGATGACCCCTCGAGGCGCACTGTCCATTTGGGCCCCACCTACATGGCCATCTCAAAA 903
 QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 DB 904 GTTCTCATCTGCCAGTTCCACTACCGAAGATGTACGAGGCGGCGCTGGACCTGTGGAA 963
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
 DB 964 CCGGAGCTGAAGACCACTACCCCTGACCCCTGTGATGATCCAAAGATTGGAGTAGCCACT 1023
 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
 DB 1024 GGCACAAAGTGTATGGCGCTGCCGATGGAGAGAGAGGATTTGTGGGCGGAGTGG 1083
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240

1084 AGCCCCATTTTCTCTCCAGACACCGCTTCTGCTCAAAAAGATGTGTGGTATCAGGG 1143
 QY 241 AenLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPro 260
 DB 1144 AACCTCTGTGGGACCGCTGGAGGAGGAACCTTTGCTTCTATGAAGGCCCCAGGGCCC 1203
 QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280
 DB 1204 TGTGTGCAGGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTCTGTGAGTCCAGAA 1263
 QY 281 GlyIleThrCysCysSerLeuLeuProSerGlyAlaGluTrpAlaArgValSerAla 300
 DB 1264 GGAATTACCTGCTGCTGCTCCCTAAATTCAGTGGGCGGAGTGGGCCAGGCTGCCGT 1323
 QY 301 ValAenAlaThrSerTrpGluProLeuThrAenLeuSerLeuValCysLeuAspSerAla 320
 DB 1324 GTCAACGCCACAAAGCTGGAGCGCTCTCAACCAACCTCTCTTTGGTCTGCTTGGATTTCAGCC 1383
 QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
 DB 1384 TCTGCCCCCGTAGCGTGGCAGTCAAGCAGCATCGCTGGGAGCAGGAGCTACTGGTGACC 1443
 QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
 DB 1444 TGGCAACCGGGCGCTGGGGAAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1503
 QY 361 ProLeuGluLysLeuAenTrpValArgLeuProProGlyAenLeuSerAlaLeuLeuPro 380
 DB 1504 CCCCTGGGAAACTCACTGGGTCCGGCTTCCCCCTGGGAACTCAGTGCTCTGTATCCA 1563
 QY 381 GlyAenPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
 DB 1564 GGGAAATTCACCTGTGCGGGTCCCTATCGAATCACTGTGCGCAGTCTCTGCTTCAGGC 1623
 QY 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
 DB 1624 TTGGCTCTGTCATCTCCGCTCTGGGGTTTCAGGGAGGAATTTAGCACCCCTAGTGGGGCCA 1683
 QY 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
 DB 1684 AGCTTTTGGGACTCCAAGATGCCCTCCAGGAGCCCCCGCCCATAGCTGGGGAGAGTTC 1743
 QY 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
 DB 1744 CCAAGGCACAGCTTCGAGGCCACCTCACCCACATACCTGTGTGCACAGAGTGGAAACC 1803
 QY 461 SerProSerValCysMetAsnValSerGlyAenThrGlnSerValThrLeuProAspLeu 480
 DB 1804 AGCCCCCTCGTCTGCATGAATGTGAGTGGCAACACACAGAGTGTCACTCCCTGACCTT 1863
 QY 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
 DB 1864 CTTGGGTGCTCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGAGGCGCCCTCTCT 1923
 QY 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
 DB 1924 GGTCCCATCTCCGCTTCATCTACAGATAACACCTCGAGGTGGAAAGTCTGCGGGGC 1983
 QY 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
 DB 1984 ATCTCTATTTCTGTGGGGCTTGTCTCTGTGGGGTGTGGCGTGGCGGACCTCTGGA 2043
 QY 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
 DB 2044 AGGTGCTACCACTTAAGGCACAAAGTGTGCCCCCTGGGTCTGGAGAAAGTCTCTGAT 2103
 QY 561 ProAlaAenSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
 DB 2104 CCTGCAACAGCAGTTTCAGGCCAGCCCCACATGGAGCAAGTACCTGAGGCCAGCCCTT 2163
 QY 581 GlyAspLeuProIleLeuGluValGluMetGluProProProValMetGluSerSer 600
 DB 2164 GGGGACTTTGCCCATCTCGAAGTGGAGGAGATGGAGCCCCCGCGGTATATGAGTCTCTCC 2223

Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
 Db 2224 CAGCCGCCAGCCAGCCGCCGCTTGACTCTGGGTATGAGAGCACTTCTGCCCCACA 2283

Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
 Db 2284 CCGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2331

RESULT 9
 ABS54548
 ID ABS54548 standard; cDNA; 2628 BP.
 AC ABS54548;
 XX 10-DEC-2002 (first entry)
 DE cDNA encoding human IL-12R-like subunit.
 KW IL-D80; human; gene; ss; cytokine; anti-inflammatory; haematopoietic;
 KW interleukin; IL-27; haematopoietic cell; immune system; inflammation;
 KW IL-12R-like subunit; interleukin 12 receptor like subunit.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 112..2022
 FT /*tag= a
 FT /product= "IL-12R-like subunit"

XX WO200268596-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-US005493.
 XX 22-FEB-2001; 2001US-00791497.
 XX 30-NOV-2001; 2001US-00000776.
 XX (SCHE) SCHERING CORP.
 XX Timans JC, Pflanz SK, Kastelein RA, Bazan JF, Rennick D;
 XX Dewaal Malefyt R, Cheung J;
 XX WPI; 2002-706978/76.
 XX P-PSDB; ABG32294.
 XX New polynucleotide and its encoded antigenic polypeptide (IL-D80
 PT cytokine), useful for regulating hematopoietic cells, in developing new
 PT therapies, or for diagnosing or treating abnormal physiology, e.g.
 PT inflammations.

XX Disclosure; Page 69-72; 74pp; English.
 XX This invention relates to the DNA and protein sequences of a new cytokine
 CC IL-D80. The protein of the invention may have antiinflammatory activity
 CC and may act as an IL-D80 modulator or an IL-27 modulator. The
 CC polynucleotide of the invention or its encoded polypeptide is useful for
 CC regulating the activation, development, differentiation or function of
 CC various cell types, e.g. haematopoietic cells. This polynucleotide or
 CC polypeptide is also useful in discovering and developing new lymphokines
 CC and their related receptor or receptor subunits, and in developing new
 CC therapies for a wide range of degenerative or abnormal conditions, which
 CC (in)directly involve the immune system or haematopoietic cells. The
 CC polynucleotide or polypeptide is useful in diagnosing or treating
 CC abnormal physiology or development, e.g. inflammations. The present
 CC sequence represents the cDNA encoding the human interleukin 12- receptor-
 CC like subunit protein of the invention

XX SQ Sequence 2628 BP; 548 A; 778 C; 790 G; 511 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 2.82e-164 Length: 2628

Score: 3494.00 Matches: 635
 Percent Similarity: 99.84% Conservative: 0
 Best Local Similarity: 99.84% Mismatches: 1
 Query Match: 99.89% Indels: 0
 DB: 6 Gaps: 0

US-10-088-950A-1 (1-636) x ABS54548 (1-2628)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
 Db 112 ATGGGGGAGGAGGGGGCCCTTCTGGCTGGCCGCTGCCAAGCTGGCGCTGCTG 171

Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
 Db 172 CCTCTGTTGGGTGCTTTTCCAGCGACGCGTCCCAGGGCAGCGCGGCCACTGCAG 231

Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 Db 232 TGTACGGAGTTGGACCCCTTGGGCGACTTGAATGCTCTGGGGAGCCCTCTTGGGAGCCTG 291

Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
 Db 292 GAGGCCCTCCGAGTTTACACTCCAGAGCCAAAGTACCGTTCCACAAACCCAGACT 351

Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 Db 352 GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGCT 411

Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120
 Db 412 GACAAACTCCTTGTCTGGGCACTAAGGAGGCGGAGCTCTCTGGCCCCCGCTTCTGCTG 471

Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
 Db 472 AACCTAGAAACCCAAATGAAGCCAAACGCCCGCTGGCGCTGACGTGGACTTTTCC 531

Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 Db 532 GAGGATGACCCCTGGGAGGCACTGTCCATTGGGCCCCACCTACATGGCCATCTCATAAA 591

Qy 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 Db 592 GTTCTGATCTGCCAGTTTCCACTACCGAAGATGTCCAGAGGCGGCTGGACCTGCTCGAA 651

Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
 Db 652 CCGAGCTGAAGACCAATACCCCTGACCCCTGTGTGAGATCCAAAGATTGGAGTAGCCACT 711

Qy 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
 Db 712 GGCTACAAAGTGTATGGCGCTGCCGATGGAGAAAGAGAGATTGTGGGCGAGTGG 771

Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
 Db 772 AGCCCACTTTTGTCTTCCAGACACCGCTTCTGTCTCCAAAAGATGTGTGGGTATCAGG 831

Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
 Db 832 AACCTCTGTGGAGCGCTGGAGGAGGAAACCTTGTCTTATGGAAGGCCCCAGGGCCCC 891

Qy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280
 Db 892 TGTGTGCAAGTGTACAAAGTCTGGTTCTGGGTTGGAGTCTGTGAGCTGAGTCCAGAA 951

Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
 Db 952 GGAATTAACCTGCTGCTCCCTAAATTCCAGTGGGCGGAGTGGCGGAGGTGCTGCGCT 1011

Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
 Db 1012 GTCACGCCACAAAGCTGGGAGCCTCTCACAACCTCTCTTGTGCTGCTTGGATTACGCC 1071

Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340

Db 1072 TCTGCCCCCGTAGCTGGCAGTCACGACATCGCTGGGAGCAGCGAGCTACTGTGTACC 1131
 Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
 Db 1132 TGGCAACCGGGCGCTGGGAACACATCGAGATGTAGTGAGCTGGGCTCGAGATGGGAC 1191
 Qy 361 ProLeuGluLeuLeuAsnTrpValArgLeuProGlyAsnLeuSerAlaLeuLeuPro 380
 Db 1192 CCCTCGGAGAACTCAACTGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1251
 Qy 381 GlyAsnPheThrValGlyValProTyArgIleThrValThrAlaValSerAlaSerGly 400
 Db 1252 GGGAAATTCACGTCTGGGGTCCCTATCGATCATCTGACCGCATCTCTGCTTCAGC 1311
 Qy 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
 Db 1312 TTGGCCTCTGCATCTCTCCCTCTGGGGTTCAGGGAGAAATTAGCACCCCTAGTGGGGCA 1371
 Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
 Db 1372 AGCTTTGGGACTCCAAAGATGCCCTCCAGGAGACCCCGCCATAGCGTGGGAGAGGTC 1431
 Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyThrLeuCysAlaGlnSerGlyThr 460
 Db 1432 CCAAGGACACAGCTTCAGGACCACTCACCTACCTTGTGTGCAGAGTGAAC 1491
 Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
 Db 1492 AGCCCTCCGCTCTGCATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCTGACCTT 1551
 Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
 Db 1552 CCTTGGGGTCCCTGTAGCTGTGGGTGAGCAGCATCTACCATCGTCGAGGCGCCCTCT 1611
 Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
 Db 1612 GGTCCCATCTCGGCTCTCATCTACAGATACACCTCGAGTGGAAATTTCTGCGGGC 1671
 Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
 Db 1672 ATCTATTCTTGGGGCTTGTTCCTGTGGGTGTGGCTGAGCTGAGCCACCTCTGGA 1731
 Qy 541 ArgCysTyThrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
 Db 1732 AGTGCTACCATCTAGGACCAAGTCTGCCCGCTGGGTCTGGGAGAAATTTCTGAT 1791
 Qy 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
 Db 1792 CTGCCCCACAGCAGTTTCAGGCCAGCCCCACATGGAGCAAGTACCTGAGCCCGCCCTT 1851
 Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600
 Db 1852 GGGGACTTCCCATCTCGAAGTGGAGGAGATGGAGCCCGCCGCTTATGAGTCTCTCC 1911
 Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyThrGluLysHisPheLeuProThr 620
 Db 1912 CAGCCGCCCGCCGACCCCGCTTGTACTCTGGGTATGAGAGCACTTCTCTGCCCA 1971
 Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
 Db 1972 CCTGAGGAGCTGGGCTTCTGGGGCCCCCGCCAGGCCACAGCTTCTGGCC 2019

RESULT 10
 ID ACA61018
 AC ACA61018 standard; cDNA; 2628 BP.

AC ACA61018;

DT 07-JUL-2003 (first entry)

DE Human T-cell cytokine receptor (TCCR) cDNA.

KW Human; interleukin; IL-D80; IL-D80; DNAX; immunosuppressive;
 KW antiinflammatory; cardiant; neutropic; neuroprotective; gene therapy;
 KW antigen; cell activation; cell development; cell differentiation;
 KW haematopoietic cell; immune disorder; T-cell immune deficiency;
 KW inflammation; tissue rejection; cardiovascular disorder; TCCR;
 KW neurophysiological condition; immunological condition; gene; ss;
 KW epsilon barr virus induced gene 3; EBI3; T-cell cytokine receptor.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 CDS 112..2022 /tag= a
 FT /product= "TCCR"
 FT /note= "T-cell cytokine receptor"
 XX US2003008343-A1.
 XX 09-JAN-2003.
 XX 22-FEB-2001; 2001US-00791497.
 XX 30-JUL-1999; 99US-0146581P.
 PR 06-AUG-1999; 99US-0147763P.
 PR 27-JUL-2000; 2000US-00627897.
 XX (TINA/) TIMANS J C.
 PA (PFLA/) PFLANZ S K.
 PA (KAST/) KASTELEIN R A.
 PA (BAZA/) BAZAN J F.
 XX Timans JC, Pflanz SK, Kastelein RA, Bazan JF;
 DR WPI; 2003-429883/40.
 DR P-PSDB; ABU09752.
 XX New substantially pure or isolated antigenic polypeptide that binds to
 PT the binding composition, useful for treating immune disorders, e.g. T-
 PT cell immune deficiencies, inflammation, tissue rejection, or
 PT cardiovascular conditions.
 XX Claim 24; Page 28-30; 39pp; English.
 CC The invention describes a substantially pure or isolated antigenic
 CC polypeptide, which binds to the binding composition comprising at least
 CC 17 contiguous amino acids from a sequence of 242, 231, 243 or 234 amino
 CC acids, fully defined in specification. The polynucleotides, polypeptides
 CC and antibodies are useful for regulating activation, development,
 CC differentiation, and functions of various cell types, including
 CC haematopoietic cells. They are also useful for treating abnormal medical
 CC conditions, including immune disorders, e.g. T-cell immune deficiencies,
 CC inflammation, tissue rejection, or cardiovascular or neurophysiological
 CC conditions. The antibodies are useful for detecting or diagnosing various
 CC immunological conditions related to expression of respective antigens.
 CC This sequence encodes human T-cell cytokine receptor (TCCR) to which the
 CC composite factor formed by IL-D80 and Epstein barr virus induced gene 3
 CC (EBI3) binds
 XX SQ Sequence 2628 BP; 548 A; 778 C; 790 G; 511 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 2,82e-164 Length: 2628
 Score: 3494.00 Matches: 635
 Percent Similarity: 99.84% Conservative: 0
 Best Local Similarity: 99.84% Mismatches: 1
 Query Match: 99.89% Indels: 0
 DB: 8 Gaps: 0

US-10-088-950A-1 (1-636) x ACA61018 (1-2628)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpProLeuProLysLeuAlaLeuLeu 20
 Db 112 ATCGGGGAGGAGGCGGGCGGCTTCTGTGGTGTGGCGCTGCCAAGCTGGCGTGTG 171

Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
Db	172	CCTCTGTGTGGTGCTTTTCAGCGGACGGCTGCCAGGGCAGCGCGGGCCACTGCAG	231
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAanCysSerTrpGluProLeuGlyAspLeu	60
Db	232	TGCTACGGAGTTGGACCTTTGGCCACTTGAATCTGCTGGGAGCCCTTTGGGGACCTG	291
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	292	GGAGCCCTCCGAGTTACACTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	351
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	352	GTGGCAGTGGCAGCCGCGAGCTGGGTGGCCATTCCTCGGGAACAGCTCACCATGTCT	411
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal	120
Db	412	GACAACTCTCTTGTCTGGGGCACTAAGGAGCGCCAGCCCTCTCTGGCCCCCGTCTTCGTG	471
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	472	AACTAGAAACCCAAATGAGCAAAACGCCGCCCGCTGGGCCCTGACGTGGACTTTTCC	531
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	532	GAGGATGACCCCTCGAGGCCACTGTCTATTTGGGCCCCACCTACATGGCCATCTCATAA	591
Qy	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaIleatTrpThrLeuLeuGlu	180
Db	592	GTTCGATCTGCGAGTTCCACTACCGAAGATGTGAGGAGCGCGCTGGACCTGTCTGAA	651
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	652	CCGGAGCTGAGACCATACCCCTGACCCCTGTGTGATCCAAAGATTTTGGAGCTAGCCACT	711
Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
Db	712	GGCTACAAAGTGTATGGCGCTGCGCGATGGAGAAAGAGAGATTTTGGGGCGAGTGG	771
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	772	AGCCCCATTTTCTCTCCAGACACCGCTTCTGCTCCAAAGATGTGTGGGTATCAGGG	831
Qy	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
Db	832	AACTCTGTGGAGCGCTGGAGGAGAGAACCTTTGCTTATGGAAAGGCCCCAGGGCCC	891
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
Db	892	TGTGTGCAGTGCAGTACAAAGTCTGTTCTGGGTGGAGGTCTGAGCTGAGTCCAGAA	951
Qy	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
Db	952	GGAAATACCTGTCTGTCTCTCCCTAATTCCTAGTGGGGCGAGTGGCGGAGTGGCGCT	1011
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
Db	1012	GTCACGCCCAAGCTGGAGGCTCTACCAACCTCTCTTTGGTCTGCTTGGATTCAGCC	1071
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
Db	1072	TCTGCCCCCGTAGCGTGGCAGTCAGCAGCATCGCTGGGAGCAGGAGCTACTGGTGACC	1131
Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
Db	1132	TGGCAACCGGGCCCTGGGGAACCACTGAGCATGTAGTGACTGGGCTCGAGATGGGGAC	1191
Qy	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
Db	1192	CCCCGGAGAACTCACTGGGTCTGGGCTCTCCCTCTGGGAACCTCAGTGTCTGTATACA	1251

Db 421 GAGGATGACCCCTGGAGGCCACTGTCATTTGGGCCCCACCTACATGGCCATCTCATAA 480
 Qy 161 ValLeuileCysGlnPheHsTyArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 Db 481 GTTCTGATCTGCCAGTTCACATACCAAGATGTGAGAGGCGGCTGGACCTGTCTGAA 540
 Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
 Db 541 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAGATTTGGAGTAGCCACT 600
 Qy 201 GlyTyLysValTyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220
 Db 601 GGCTACAAAGTGTATGGCGCTGCCGATGGAGAGAGAACTTTGCTTATGGAGGCCCGAGTGG 660
 Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
 Db 661 AGCCCCATTTGTCCTTCAGACACCGCTTGTCTCCAAAGATGTGGGTATACAGG 720
 Qy 241 AsnLeuCysGlyThrProGlyGlyGluProLeuLeuLeuTrpLysAlaProGlyPro 260
 Db 721 AACCTCTGTGGAGCGCTGGAGAGAGAACTTTGCTTATGGAGGCCCGAGGCC 780
 Qy 261 CysValGlnValSerTyLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
 Db 781 TGTGTGAGGTGAGCTACAAAGTCTGGTTCTGGTTGGAGGTCTGTGAGTCCAGAA 840
 Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
 Db 841 GGAATTTACCTGTGCTGCTCCCTTAATTCAGTGGGCGGAGTGGGCCAGGGTTCGGCT 900
 Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
 Db 901 GTCAACGCCACAAAGCTGGAGGCTCTCACCACTCTCTTTGGTCTGTGGATTGAGCC 960
 Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
 Db 961 TCTGCCCCCTAGCTGGAGTGCAGTGCAGCAGCTGCTGGAGCAGCAGGACTCTGGTAC 1020
 Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
 Db 1021 TGGCAACCGGGGCTGGGAAACCACTGGAGCATGTAATGAGCTGGGCTCGAGATGGGAC 1080
 Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
 Db 1081 CCCTGGAGAACTCACTGGGTCCGGCTTCCCTGGGAACTCAGTCTCTGTATCA 1140
 Qy 381 GlyAsnPheThrValGlyValProTyArgIleThrValThrAlaValSerAlaSerGly 400
 Db 1141 GGGAAATTCACGTGCGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1200
 Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
 Db 1201 TTGGCTCTGCACTCCCTGCTGGGGTTCAGGGAGAAATGACCCCTAGTGGGGCCA 1260
 Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
 Db 1261 ACGCTTTGGGACTCCAAAGTCCCTCAGGACCCCGCATAGCTGGGGAGAGGTCT 1320
 Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyThrLeuCysAlaGlnSerGlyThr 460
 Db 1321 CCAAGGCACGAGCTTCAGGCGCCACTCACCCACTACACCTTGTGTGCACAGAGTGAACC 1380
 Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
 Db 1381 AGCCCCCTCGCTGCAATGAATGTGAGTGGCAACACAGAGTGTACCTGCTGACCTT 1440
 Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
 Db 1441 CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT 1500
 Qy 501 GlyProIleLeuArgIleuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
 Db 1501 GGTCCCATCTCCGGCTTCTATCTACAGATTAACACCTGAGGTGGAAGTCTTCTGCGGCG 1560

Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
 Db 1561 ATCTTATTTCTTGTGGGGCTTGTCTCTTGGGTGTGGCTGAGCTGGCCACCTCTGA 1620
 Qy 541 ArgCysTyHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
 Db 1621 AGGTGCTACCACTAAGGCACAAAGTGTGCCCCCTGGTCTGGGAGAAAGTCTCTGAT 1680
 Qy 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
 Db 1681 CTTGCAACAGCAGTTCAGGCCAGCCCACTGGAGCAAGTACCTGAGGCCAGCCCTT 1740
 Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600
 Db 1741 GGGGACTTCCCATCTCGAAGTGGAGAGATGGAGCCCCCGCGGTTATGGAGTCTTCC 1800
 Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyTrpGluLysHisPheLeuProThr 620
 Db 1801 CAGCCCGCCAGGCCACCGCCGCTTGACTCTGGGTATGAGAAGCACTTCTCTGCCACA 1860
 Qy 621 ProGluGluLeuGlyLeuGlyProProArgProGlnValLeuAla 636
 Db 1861 CTTGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 1908

RESULT 13
 ACC46162
 ID ACC46162 standard; cDNA; 2350 BP.
 XX ACC46162;
 DT 02-JUN-2003 (first entry)
 XX Human dithp receptor-encoding cDNA.
 DE Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteome analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging; receptor; gene;
 SS.
 KW Homo sapiens.
 OS
 XX WO200297031-A2.
 XX 05-DEC-2002.
 XX 27-MAR-2002; 2002WO-US010056.
 XX 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David WH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX WPI; 2003-129518/12.
 DR P-PSDB; ABR41219.
 XX

PT Novel human diagnostic and therapeutic polypeptide useful for identifying
 PT test compound which specifically binds to a polypeptide encoded by human
 PT diagnostic and therapeutic polynucleotide, and to induce antibodies.

PS Claim 2; SEQ ID NO 83; 591pp; English.

XX
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
 CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
 CC polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
 CC detecting dithp nucleotides and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a dithp cDNA encoding a DITHP protein
 CC which has receptor activity. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 2350 BP; 455 A; 712 C; 719 G; 464 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-23e-160 Length: 2350
 Score: 3419.50 Matches: 633
 Percent Similarity: 95.34% Conservative: 1
 Best Local Similarity: 95.19% Mismatches: 2
 Query Match: 97.76% Indels: 31
 DB: 8 Gaps: 1

US-10-088-950A-1 (1-636) x ACC46162 (1-2350)

Qy 1 MetArgGlyGlyArgGlyAlaProPheThrLeuTrpProLeuProLysLeuAlaLeuLeu 20
 Db 49 ATGGGGGAGGCGAG-GGCGCCCCCTTCTGGCTGTGGCGGCTGCCCAAGCTGGCGTCTG 107
 Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
 Db 108 CCTGTGTGTGGTGTCTTTTCCAGCGACGCGTCCCCCA-GGCGAGCGCGGCCACTGCAG 166
 Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 Db 167 TGCTACGGAGTTGACCCCTTGGGGGACTTGAACCTGCTGCTGGGGAGCCCTTTGGGGACCTG 226
 Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
 Db 227 GGAGCCCCCTCCGAGTTACACCTCCAGCGCCAAAGTACCGTTCCACAAACCCAGACT 286
 Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 Db 287 GTGGCAGTGGCGCGGACGAGCTGGGTGGCCATTCTCTGGGAAACAGCTCACCATGTCT 346
 Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120
 Db 347 GACAAATCTCTTGTCTGGGGGACTTAAGGCGAGGCGAGCCTCTCTGGCCCCCGCTTCTGCTG

Qy 121 AsnLeuGluThrGln----- 125
 Db 407 AACCTAGAAACCCCAAGTAACGTGTCAGGAGGGTGGCGCTCTATATGGGGGTGGGTGCTC 466
 Qy 126 -----MetLysProAsnAlaPro 131
 Db 467 TTGGAGGGCGTGGTCTACTACACCTAGTTTCCCTTCCCGAGTGAAGCCAAACGCCCC 526
 Qy 132 ArgLeuGlyProAspValAspPheSerGluAspProLeuGluAlaThrValHisTrp 151
 Db 527 CGCTGGGCGCTGACGTGGACTTTTCCGAGGATGACCCCTGGAGGCCACTGTCCATTGG 586
 Qy 152 AlaProProThrTrpProSerHisLysValLeuLysCysGlnPheHisTyrArgArgCys 171
 Db 587 GCGCCACCTACATGGCCATCTCTAAAGTTCTGATCTGCCAGTTCCATACCGAAGATGT 646
 Qy 172 GlnGluAlaAlaTrpThrLeuLeuGluProGluLeuLysThrIleProLeuThrProVal 191
 Db 647 CAGAGGCGGCGCTGGACCCCTGCTGGAAACCGGAGCTGAAGACCATACCCCTGACCCCTGT 706
 Qy 192 GluIleGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGlu 211
 Db 707 GAGATCCAAGATTGGAGCTAGCCACTGGCTACAAAGTGTATGGCCGCTGCCGAGTGGAG 766
 Qy 212 LysGluGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSer 231
 Db 767 AAAGAGAGGATTGTGGGCGAGTGGAGGCCCATTTTGTCTTCCACAGACACCGCTTCT 826
 Qy 232 AlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluPro 251
 Db 827 GCTCCAAAAGATGTGGGTATCAGGGAACCTCTGTGGGACGCTGGAGGAGGAGAACCT 886
 Qy 252 LeuLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTrp 271
 Db 887 TTGCTTCTATGGAGGCGCCCGAGGCCCTGTGTGCGAGGTGAGCTACAAAGTCTGGTCTGG 946
 Qy 272 ValGlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuLeuLeuProSer 291
 Db 947 GTTGGAGTCTGTGAGCTGAGTCCAGAGGAATTAACCTGTCTGTCTCCCTAAATCCCACT 1006
 Qy 292 GlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAsn 311
 Db 1007 GGGGCGGAGTGGCGCCAGGGTGTCCGTGTCAACGCCAACAGCTGGGAGCTCTCACCAC 1066
 Qy 312 LeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerile 331
 Db 1067 CTCTCTTGTGCTGTGGATTGAGCTCTGCCCGCCGTTAGCTGGAGCTCAGCAGCATC 1126
 Qy 332 AlaGlySerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGluHis 351
 Db 1127 GCTGGGAGCACGAGCTACTGTGTGACCTGGCAACCGGGGCTGGGGAACCACTGGAGCAT 1186
 Qy 352 ValValAspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuPro 371
 Db 1187 GTAGTGGACTGGGCTCGAGATGGGACCCCTCGAGAAACTCACTGGGTCCGCTTCCC 1246
 Qy 372 ProGlyAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIle 391
 Db 1247 CTTGGGAACCTCAGTGTCTGTGTACAGGGAATTTACTGTGGGGTCCCTATTCGAATC 1306
 Qy 392 ThrValThrAlaValSerAlaSerGlyLeuAlaSerAlaSerSerValTrpGlyPheArg 411
 Db 1307 ACTGTGACCGCAGTCTCTGCTTCCAGCTTGGCCTCTGCATCTCTCCGTCTGGGGTTCCAG 1366
 Qy 412 GluGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGly 431
 Db 1367 GAGGAATTAAGCACCCCTAGTGGGGCCCAACGCTTTGGCGACTCCCAAGATGCCCTCCAGGG 1426
 Qy 432 ThrProAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHis 451
 Db 1427 ACCCCGCCCAACAGCTGGGAGAGGTCCTCCAGGACACAGCTTCGAGGCCACCTCACCAC 1486
 Qy 452 TyrThrLeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsn 471


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Db 1487 TACACCTTGTGTGCAGAGTGGAAACCGCCCTCGTCTGCATGAATGTGAGTGGCAAC 1546
Qy 472 ThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAla 491
Db 1547 ACACAGAGTGTACACCTGTGCTGACCTTCTTGGGGTCCCTGTGAGCTGTGGGTGCAGCA 1606
Qy 492 SerThrIleAlaGlnGlyProGlyProGlyProGlyProGlyProGlyProGlyProGly 511
Db 1607 TCTACCATCGCTGGAGAGGCGCTCTGTGTCCATCTCCGCTTCACTACAGATAC 1666
Qy 512 ThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuGly 531
Db 1667 ACCCTGAGTGGAAAGTCTTGGCGGCACTTCTTCTTGGGGTGTCTGTGGGG 1726
Qy 532 CysGlyLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArgHisLysValLeuPro 551
Db 1727 TGTGGCTGAGCTGGCCACCTCTGGAAGTGTCTACCACTAAGGCACAAAGTGTGCTGCC 1786
Qy 552 ArgTrpValTrpGluLysValProAspProAlaAsnSerSerSerGlyGlnProHisMet 571
Db 1787 CGTGGGTCTGGAGAAAGTCTCTGATCTCTGCCACAGCAGTTCAGCGCCAGCCCAATG 1846
Qy 572 GluGlnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGluMet 591
Db 1847 GAGCAAGTACCTGAGCGCCAGCCCTTGGGACTTGGCCATCTTGGAACTGGAGGATG 1906
Qy 592 GluProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeuAspSer 611
Db 1907 GAGCCCCCGCGGTATGAGTCTCTCCAGCCGCTCCAGCCGCGCCAGCCAGCCGCTGACT 1966
Qy 612 GlyTyrGluLysHisPheLeuProThrProGluGluLeuGlyLeuGlyProProArg 631
Db 1967 GGGTATGAGAGACACTTCTGCCACACCTGAGGAGCTGGGCTTCTGGGGCCCCCAGG 2026
Qy 632 ProGlnValLeuAla 636
Db 2027 CCACAGTCTTGCC 2041
RESULT 14
AAT94119
ID AAT94119 standard; cDNA; 2368 BP.
AC AAT94119;
XX
XX 22-MAY-1998 (first entry)
XX Human haematopoietic cytokine receptor Zcytor1 cDNA.
XX Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;
XX cancer diagnosis; agonist; antagonist; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 23..1759
XX /*tag= a
XX /product= "Zcytor1"
XX
XX WO9744455-A1.
XX
XX 27-NOV-1997.
XX
XX 19-MAY-1997; 97WO-US008502.
XX
XX 23-MAY-1996; 96US-00653740.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
XX WPI; 1998-018509/02.
XX
XX P-PSDB; AAW33398.
```

```
XX Haematopoietic cytokine receptor - useful for ligand detection, and
PT pathological condition diagnosis.
XX Claim 13; Page 39-43; 86pp; English.
PS
XX The present sequence encodes the human haematopoietic cytokine receptor
CC Zcytor1, useful for ligand detection, and pathological condition
CC diagnosis, including cancer. Receptor agonists of the protein can be used
CC to stimulate the proliferation and development of target cells in vitro
CC and in vivo. The agonists can stimulate cell mediated immunity and
CC lymphocyte proliferation, to treat infection involving immunosuppression,
CC e.g. viral infections. They may also be used to suppress tumours, induce
CC cytotoxicity, treat leukaemias and enhance the regeneration of the T-
CC cell repertoire after bone marrow transplantation. Antagonists of the
CC protein may be used to suppress the immune system, treat autoimmune
CC diseases, including rheumatoid arthritis, multiple sclerosis and diabetes
CC mellitus. Immune suppression caused by the antagonists can also be used
CC to reduce rejection of tissue or organ transplants and grafts, and to
CC treat T-cell specific leukaemias and lymphomas
XX Sequence 2368 BP; 506 A; 688 C; 701 G; 473 T; 0 U; 0 Other;
SQ
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Alignment Scores:

Pred. No.:	2,82e-147	Length:	2368
Score:	3150.00	Matches:	578
Percent Similarity:	90.88%	Conservative:	0
Best Local Similarity:	90.88%	Mismatches:	0
Query Match:	90.05%	Indels:	58
DB:	2	Gaps:	1

US-10-088-950A-1 (1-636) x AAT94119 (1-2368)

Qy	1	MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
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Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
Db	83	CCTCTGTTGGTGCTCTTTCCAGCGGACGGCTCCAGGGGAGCGCGGGCCATCGAG	142
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	143	TGCTACGGAGTTGGACCTTGGCGACTTGAACCTCTCGTGGAGCCTCTTGGGACCTG	202
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	203	GGAGCCCCCTCGAGTTACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	262
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	263	GTGGCAGTGGGAGCGGAGCGGAGCTGGTGGCCATCTCTGGGAACAGCTACCATGCT	322
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
Db	323	GACAACTCCTTGTCTGGGGCACTAAGGCAGGCCAGCCTCTCTGGCCCCCGCTTCGGT	382
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	383	AACCTAGAAACCCAAATGAAGCCAAACGCCCGCGCTGGGCGCTTTCCTTC	442
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	443	GAGGATGACCCCTGGAGGCCACTGTCTATTGGGGCCCCCACCCTACATGGCCATCTATAA	502
Qy	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaThrThrLeuLeuGlu	180
Db	503	GTTCGTGATCTGCCAGTTCACCTACCGAAGATGTCCAGGAGGCGGCGCTGGACCTGTGAA	562
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluAlaThr	200
Db	563	COGGAGCTGAAGACCATACCCCTGTGATCCCAAGATTGGAGTAGGAGTGCACCT	622

QY GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220
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QY SerProLeuLeuSerPheGlnThrProProSerAlaProLysAspValTyrValSerGly 240
Db AGCCCAATTTGTCTCTCCACACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 742
QY AsnLeuGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
Db AACCTCTGTGGAGCGCTGGAGGAGAGAACTTTGCTTCTATGGAAGGCCCCAGGGGCC 802
QY CysValGlnValSerTyrLysValTyrPheTrpValGlyArgGluLeuSerProGlu 280
Db TGTGTGAGGAGTACAAAGTCTGGGTCTGGGTCTGGAGTCTGAGTCTGAGTCCAGAA 862
QY GlyTyrThrCysCysSerLeuLeuProSerGlyAlaGluTrpAlaAtrGValSerAla 300
Db GGATTAACCTGCTGCTGCTCTCTAATTCCTAGTGGGGCGAGTGGCCAGGGTGTCCGCT 922
QY ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
Db GTCAACGCCACAAGCTGGAGCCCTCTACCAACCTCTCTTTGGTCTGCTTGGATTACGCC 982
QY SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
Db TCTGCCCCCGTAGCTGGCAGTCAGCAGCATCTGCGGAGCAGCGACTACTGCTGACC 1042
QY TrpGlnProGlyProGlyGluProLeuGluHisValValAspTyrAlaAtrGAspGlyAsp 360
Db TGGCAACCGGGGCTGGGGAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGGAC 1102
QY ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
Db CCCCTGGAGAACTCACTGGGTCCGGCTCCCGCTGGGAACCTCAGTGTCTGTACCA 1162
QY GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db GGGAAATTTCACTGTCGGGGTCCCTATCGAATCACTGTACCGCAGTCTCTGCTTCAGGC 1222
QY LeuAlaSerAlaSerValTyrGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db TTGGCCCTCTGCATCTCCGCTCGGGGTTCAGGAGGAATTAGCACCCCTAGTGGGGCCA 1282
QY ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db ACGCTTTGGGACCTCCAGATGCCCTCCAGGACCCCGCCATAGCTGGGGAGAGTTC 1342
QY ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db CCAAGGCACCAAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGAACC 1402
QY SerProSerValCysMetAsnValSerCysAsnThrGlnSerValThrLeuProAspLeu 480
Db AGCCCTTCGCTGCTCATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCTGACCTT 1462
QY ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db CTTGGGGTCCCTGTGAGCTGTGGGTACAGCATCTACCATCGTGTGACAGGGCCCTCT 1522
QY GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db GGTCCCATCTCCGGCTTCTATACACAGATAACACCTGAGGTGAAAGTTCTTCCGGGCG 1582
QY IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db ATCCTATTCTTGTGGGCTTGTCTCTGTGGGTGTGGCTGAGCTGGCCACCTCTGGA 1642
QY ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db AGTGTCTACCACTTACGACCAAGATCTGCCCCGCTGGGTCTGGGAGAAAGTTCTTGAT 1702
QY ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580

Db ||||| 1703 CCTGCCAACAGCATTCAC----- 1720
QY 581 GlyAspLeuProIleLeuGluValGluMetGluProProValMetGluSerSer 600
Db 1720 ----- 1720
QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1720 ----- 1720
QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1721 -----GGCCTTCTGGGGCCCCCAGGACAGAGTTCTGGCC 1756

RESULT 15

ADR20078
ID ADR20078 standard; cDNA; 1835 BP.
XX AC ADR20078;
XX XX 07-OCT-2004 (first entry)
XX DE Human immune response associated protein (IRAP) cDNA, seq id 38.
XX KW Neuroprotective; anorectic; cytostatic; gene therapy;
KW human immune response associated protein; IRAP; immune system;
KW neurological; developmental; muscle; cell proliferative; disorder;
KW lipid metabolism; obesity; breast; colon; lung; ovarian; prostate;
KW cancer; gene; ss.
XX OS Homo sapiens.
XX PN WO2004048550-A2.
XX PD 10-JUN-2004.
XX XX 25-NOV-2003; 2003WO-US038178.
XX PF 26-NOV-2002; 2002US-0429442P.
XX PR 27-NOV-2002; 2002US-0429839P.
XX PR 13-JAN-2003; 2003US-0439946P.
XX PR 07-FEB-2003; 2003US-0446182P.
XX (INCY-) INCYTE CORP.
XX PA Tran UK, Richardson TW, Becha SD, Elliott VS, Swarnakar A;
XX PI Lee SY, Ramkumar J, Wang JT, Chien D, Murage J, Gera M, Marquis JP;
XX PI Chawla NK, Nakamura LL, Kable AE;
XX DR WPI; 2004-450368/42.
XX DR P-PSDB; ADR20046.
XX XX New immune response associated protein, useful in diagnosing, treating,
PT or preventing obesity, cancer, immune system, neurological,
PT developmental, muscle, or cell proliferative disorders, or disorders of
PT lipid metabolism.
XX XX Claim 5; SEQ ID NO 38; 199pp; English.
XX CC The invention relates to an isolated polypeptide with human immune
CC response associated protein (IRAP) activity. Further disclosed are
CC polynucleotides encoding the polypeptides of the invention. The
CC polypeptides, polynucleotides, composition, and methods are useful in
CC diagnosing, treating, or preventing immune system, neurological,
CC developmental, muscle, or cell proliferative disorders, disorders of
CC lipid metabolism, obesity, and breast, colon, lung, ovarian, or prostate
CC cancer. The current sequence represents a human immune response
CC associated protein encoding cDNA.
XX SQ Sequence 1835 BP; 331 A; 568 C; 568 G; 368 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,06e-147 Length: 1835
 Score: 3144.50 Matches: 579
 Percent Similarity: 91.37% Conservative: 3
 Best Local Similarity: 90.89% Mismatches: 1
 Query Match: 89.89% Indels: 54
 DB: 12 Gaps: 1

US-10-088-950A-1 (1-636) x ADR20078 (1-1835)

QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
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 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
 DB 97 CCTCTGTGTGGTGTCTTTTCAGCGGAGCGCTGCCAGGGCAGCCCGGGCCACTGCGAG 156
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 DB 157 TGCTACGGAGTTGGACCTTTGGGCGACTTGAACCTGCTGTGGGAGCCTCTTGGGGACCTG 216
 QY 61 GlyAlaProSerGlnLeuHisLeuGlnSerGlnLysTyr-ArgSerAsnLysThrGlnTh 80
 DB 217 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTATGAAG----- 259
 QY 80 rValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSe 100
 DB 259 ----- 259
 QY 100 rAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVa 120
 DB 259 ----- 259
 QY 120 laenLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSe 140
 DB 260 -----CCAAACGCCGCCCGGCTGGGCCCTGAGCGTGGACTTTTC 297
 QY 140 rGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisly 160
 DB 298 CGAGGATGACCCCTGAGGCCACTGTCCATTTGGGCCCCACCTACATGGCCATCTCATAA 357
 QY 160 sValLeuileCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGl 180
 DB 358 AGTTCTGATCTGCCAGTTCCACTTACCGAAGATGTGAGGAGGCGGCTGGACCTGTCTGA 417
 QY 180 uProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaTh 200
 DB 418 ACCGGAGCTGAAGACCATACCCCTGACCCCTGTGAGATCCAAAGATTTGGAGCTAGCCAC 477
 QY 200 rGlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTr 220
 DB 478 TGGCTACAAGTGTATGGCGCTGCCGATGGGAAAGAGAGGATTTGTGGGCGAGTG 537
 QY 220 pSerProileLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGl 240
 DB 538 GAGCCCCATTTGTCTCTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGTATCAGG 597
 QY 240 yAenLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPr 260
 DB 598 GGACCTCTGTGGGACCCCTGGAGGAGGAAACCTTTGCTTCTATGGAAGGCCCCAGGGCC 657
 QY 260 oCysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGl 280
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 DB 718 AGGAATTACCTGTCTGTCTCCCTAATTTCCAGTGGGGCGGAGTGGGCCAGGGTGTCCGC 777
 QY 300 aValAenAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAl 320
 DB 778 TGTCAACGCCCAAGCGGAGGCTCTCCAAACCTCTCTTTGGTCTGCTTGGATTTCAGC 837

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 DB 898 CTGGCAACCGGGGCTTGGGAAACCACTGAGCATGTAGTGGAGTGGGCTCGAGATGGGA 957
 QY 360 pProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPr 380
 DB 958 CCCCTGGAGAAACTCAACTGGGTCGGCTTCCCTTGGAAACCTCAGTGTCTGTATTACC 1017
 QY 380 oGlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGl 400
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 QY 400 yLeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPr 420
 DB 1078 CTGTGGCCTCTGCATCTCGTCTGGGGTTTCAGGAGGAATTAGCACCCCTAGTGGGGCC 1137
 QY 420 oThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyLysVa 440
 DB 1138 AACGCTTTGGGACATCCGAGATGCCCTTCCAGGGACCCCGCCATAGCGTGGGAGAGGT 1197
 QY 440 lProArgHisGlnLeuLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyTh 460
 DB 1198 CCCAAGGCCACAGCTTCGAGGCCACTCACCCACTACACCTTGTGTGCACAGTGGAAAC 1257
 QY 460 rSerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLe 480
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 QY 480 uProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPr 500
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 QY 500 oGlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGl 520
 DB 1378 TGGTCCCATCTCCGGCTTCATCTACCAGATPAACACCTGAGTGGAAAGTTCTGCCGGG 1437
 QY 520 yIleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGl 540
 DB 1438 CATCTATTCTTGTGGGGCTTGTCTGTGGGTGTGGCTGAGCTGGCCACCTCTGG 1497
 QY 540 yArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAs 560
 DB 1498 AAGGTGTACCACTTAAGGCACAAAGTGTGCCCGCTGGGTCTGGGAAAGTTCTCTGA 1557
 QY 560 pProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLe 580
 DB 1558 TCCTGCCAACAGCAGTTCAGGCCAGCCCCACATGGAGCAAGTACCTGAGGCCAGCCCT 1617
 QY 580 uGlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSe 600
 DB 1618 TGGGAGCTTGGCCATCTCGAAGTGGAGAGATGGAGCCCGCCGCGTGTATGGAGTCTTC 1677
 QY 600 rGlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProTh 620
 DB 1678 CCAGCCCGCCAGGCCACCGCCCTGACTCTGGGTATGAGAAGACCTTCTCTGCCAC 1737
 QY 620 rProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
 DB 1738 ACTGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTTGGCC 1786

Search completed: February 23, 2005, 05:20:05
 Job time : 987 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3498	100.0	2663	1	US-08-653-740-4	Sequence 4, Appli
2	3498	100.0	2663	2	US-09-073-594-4	Sequence 4, Appli
3	3498	100.0	2663	3	US-09-275-925-4	Sequence 4, Appli
4	3150	90.1	2368	1	US-08-653-740-2	Sequence 2, Appli
5	3150	90.1	2368	2	US-09-073-594-2	Sequence 2, Appli
6	3150	90.1	2368	3	US-09-275-925-2	Sequence 2, Appli
7	2044	58.4	2589	1	US-08-653-740-6	Sequence 6, Appli
8	2044	58.4	2589	2	US-09-073-594-6	Sequence 6, Appli
9	2044	58.4	2589	3	US-09-275-925-6	Sequence 6, Appli
10	381.5	10.9	4040	2	US-08-685-118-1	Sequence 1, Appli
11	381.5	10.9	4040	1	US-08-915-495-1	Sequence 1, Appli
12	381.5	10.9	4040	2	US-08-914-520-1	Sequence 1, Appli

; INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:; INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:

; LENGTH: 2663 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 139...2049
 ; US-08-653-740-4

Alignment Scores:

Pred. No.: 1,15E-270 Length: 2663
 Score: 3498.00 Matches: 636
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-088-950A-1 (1-636) x US-08-653-740-4 (1-2663)

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 DB 199 CTTCTGTTGGGTGCTTTTCCAGCGGACGCTGCCAGGCGAGCGCCGGGCCACTGGCAG 258
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAenCysSerTrpGluProLeuGlyAspLeu 60
 DB 259 TGTCTACGAGTGGACCCCTTGGCGGACTTGAACCTGCTGGGAGGCTCTTGGGACCTG 318
 QY 61 GlyAlaProSerLeuLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
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 DB 739 GGCTACAAAGTGTATGGCCGCTGCCGATGGAGAGAGAGATTGTGGGGCGGAGTGG 798
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 QY 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
 DB 1639 GGTCCCATCTCGGCTTCACTACAGATAACACCCCTGAGGTGGAAGTTCTGCCAGGC 1698
 QY 521 IleLeuPheLeuTrpGlyPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
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Db 1999 CCTGAGAGAGTGGGCGCTTCTGGGGGCCCCCCCCAGGCCACAGGTTCGTGGCC 2046

RESULT 2

US-09-073-594-4
; Sequence 4, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sorecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..2049
US-09-073-594-4

Alignment Scores:
Pred. No.: 1.15e-270 Length: 2663
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-088-950A-1 (1-636) x US-09-073-594-4 (1-2663)

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Db 199 CCTCTGTGTGGGTGCTTTCCAGCGGACGGCTCCCGAGGGGAGCGCGGCCCACTGCGAG 258
Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 259 TGCTACGGAGGTGGACCCCTTGGGCGACTTGAACCTGCTGCTGGAGGCTCTTGGGGACCTG 318
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Db 559 GAGGATGACCCCTGGAGGCCACTGTCACTTGGGCCCCACCTACATGATGCCCATCTCATAA 618
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Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuLeuAlaThr 200
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RESULT 3

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US-09-275-925-4
; Sequence 4, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E.
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673

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; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..2049
; US-09-275-925-4
Alignment Scores:
Pred. No.: 1.15e-270 Length: 2663
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-088-950A-1 (1-636) x US-09-275-925-4 (1-2663)
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Db 1879 GGGACTTGGCCATCTCTGGAAGTGGAGAGATGAGAGCCCGCCCGCTTATGAGAGTCTCTCC 1938
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1939 CAGCCCGCCAGGCCACCGCCCGCTTGACTCTGGGTATGAGAAGCACTTCTCTGCCACCA 1998

Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
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RESULT 4

US-08-653-740-2
; Sequence 2, Application US/08653740
; Patent NO. 5792850
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,740
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..1759
US-08-653-740-2

Alignment Scores:
Pred. No.: 7,92e-243 Length: 2368
Score: 3150.00 Matches: 578
Percent Similarity: 90.88% Conservative: 0
Best Local Similarity: 90.88% Mismatches: 0
Query Match: 90.05% Indels: 58
DB: 1 Gaps: 1

US-10-088-950A-1 (1-636) x US-08-653-740-2 (1-2368)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 23 ATGCGGGGAGGAGGAGGGCGCCCTTCTGGCTGTGCGCGCTGCCAAGCTGGGGCTGCTG 82
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 83 CCTCTGTGTGGGTGCTTTTCCAGCGAGCGCGTCCCGAGGCGAGCGCGGCCACGTGAG 142
Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 143 TGCTACGGATGGACCCCTTGGGCGACTTGAACCTGCTCGTGGGAGCCTCTTGGGGACCTG 202

61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
161 ValLeuLeuLeuGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluAlaThr 200
201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGlnTrp 220
221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
261 CysValGlnValSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
281 GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuValThr 340
341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440

203 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCAAACAAACCCAGACT 262
81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
263 GTGGCAGTGGCAGCCGACGAGCTGGGTGGCCATTCCTCGGGAACAGCTCACCATGTCT 322
101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
323 GACAAACTCCTTGTCTGGGGCACTAAGGAGCCAGCCCTCTCTGGCCCCCTCTTCGCG 382
121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
383 AACCTAGAAACCAATGAAGCAACAGCCCCCGCTGGGCCCTGACGTGGACTTTTCC 442
141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
443 GAGGATGACCCCTGGAGGCCACTGTGCCATTGGGCCCCACCTACATGGCCATCTCATAA 502
161 ValLeuLeuLeuGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
503 GTTCTGATCTGCCAGTTCCACATCCGAGATGTACAGAGCGGCCCTGGACCTGCTGGAA 562
181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluAlaThr 200
563 CCGGAGCTGAAGACCATACCTGACCCCTGTGAGATCCAGATTCAGAGTAGCCACT 622
201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGlnTrp 220
623 GGCTACAAAGTGTATGGCCGCTCCCGATGGAGAAAGAGAGATTTGTGGGGCGAGTGG 682
221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
683 AGCCCAATTTTGTCTTCCAGACACCGCCCTTCTGCTCCAAAAGATGTGGGTATCAGG 742
241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
743 AACCTCTGGGAGCGCTCGAGAGAGAGAACTTTGCTTCTATGGAAGCCCCAGGGCCC 802
261 CysValGlnValSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
803 TGTGTGACGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTCTGAGTGGAGTCCAGAA 862
281 GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
863 GGAATTAATCTGTCTGTCTCCCTTAATCCAGTGGGGCGAGTGGCCAGAGGTGCCGT 922
301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
923 GTCAACGCCACAAAGCTGGGAGCTCTCACCAACCTCTCTTTGCTGTGCTTGGATTACGC 982
321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuValThr 340
983 TCTGCCCCCCCTAGCGTGGCAGTCAAGCAGATCGCTGGGAGCAGCGAGCTACTGTGACC 1042
341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
1043 TGGCAACCGGGGCTGGGAACACCTGGAGCATGTAGTGGACTGGGCTCGAGTGGGGAC 1102
361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
1103 CCCCTGGAGAAATCAACTGGGTGGGCTTCCCTGGGAACCTCAGTGTCTGTATTACCA 1162
381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
1163 GGAATTTTCACTGTCCGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTCTTCAGGC 1222
401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
1223 TTGGCCCTCTGCATCTCCCTCTGGGGGTTTCAGGAGGAATTAGACCCCTAGTGGGGCA 1282
421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440

1283 ACGCTTTGGGACTCCAAGATGCCCTCCAGGAGCCCGCCAGTAGCGTGGGAGAGGTC 1342
441 ProArgHisGlnLeuAtrgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
1343 CCAAGGACCAAGTTCGAGGGCCACCTCACCCACATACACCTTGTGTGTCACAGAGTGAACC 1402
461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
1403 AGCCCTCTCGTCTGCATGATGTGAGTGGCAACACACAGAGTGTACACCTGCCTGACCTT 1462
481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
1463 CTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGAGAGGCCCTCCT 1522
501 GlyProIleLeuAtrgLeuHisLeuProAspAsnThrLeuAtrgTrpLysValLeuProGly 520
1523 GGTCCCATCTCCCGGCTTCATCTACCAATACACCTCGAGGTGGAAGTTCTGCGGGC 1582
521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
1583 ATCTATTTCTGTGGGGCTTGTCTCTGTGGGTGTGGCTGAGCTGGCCACCTCTCGA 1642
541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
1643 AGGTGCTACCACTAAGGCACAAAGTACTGCCCGCTGGGTCTGGGAGAAAGTTCTCGAT 1702
561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
1703 CTGCAACAGCAGTTCA----- 1720
581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600
1720 ----- 1720
601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
1720 ----- 1720
621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
1721 -----GGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 1756

RESULT 5

US-09-073-594-2
; Sequence 2, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sorecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648

REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6673

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2368 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 23..1759

US-09-073-594-2

Alignment Scores:

Pred. No.:	7,92e-243	Length:	2368
Score:	3150.00	Matches:	578
Percent Similarity:	90.88%	Conservative:	0
Best Local Similarity:	90.88%	Mismatches:	0
Query Match:	90.05%	Indels:	58
DB:	2	Gaps:	1

US-10-088-950A-1 (1-636) x US-09-073-594-2 (1-2368)

Qy	1	MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
Db	23	ATGGGGGAGGACGGGGCCCTTTCTGGGTGTGGCGTGTGCCAAGCTGGCGCTGCTG	82
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlnSerAlaGlyProLeuGln	40
Db	83	CCTCTGTGTGGGTGCTTTTCCAGCGGACGGCGTCCCCAGGGGACGGCGGCCACTGCAG	142
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuasnCysSerTrpGluProLeuGlyAspLeu	60
Db	143	TGCTACCGAGGTGACACCTTGGGGGACTTGAACCTGCTCGTGGGAGCCTCTTGGGGACCTG	202
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	203	GGAGCCCTCCGAGTTACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	262
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	263	GTGGCAGTGGCAGCGGAGGAGCTGGGTGGGCCATTCTCGGGAACAGCTCACCATGTCT	322
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
Db	323	GACAAACTCCTGTGTGGGGCAGCTAAGGCAGGCCAGCCCTCTCTGGCCCCCGCTTCGTG	382
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	383	AACCTAGAACCCCAATGAAGCCAAACGCCCGCTGGGCCCTGACGTGGACTTTTCC	442
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	443	GAGGATGACCCCTGGAGGCACCTGTCCATTGGGCCCCACCTACATGGCCATCTCATAA	502
Qy	161	ValLeuLeuCysGlnPheHisTyrArgArgCysGlnGluAlaIleTrpThrLeuLeuGlu	180
Db	503	GTTCTGATCTGCCAGTTCACATACCGAAGATGTCCAGGAGCGCGCTGGACCTGTGGAA	562
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	563	CCGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAAGATTTGGAGCTAGCCACT	622
Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
Db	623	GGCTACAAAGTGTATGGCGCTGCGGATGGAGAAAGAGAGATTTGTGGGGCGAGTGG	682
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	683	AGCCCCATTTGTCTTCCAGACACCGCCTTCTGCTCCAAAGATGTGTGGGTATCAGGG	742

Qy	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
Db	743	AACCTCTGTGGAGCGCTTGGAGGAGAGAACCTTTGTTCTATATGGAAGGCCCCAGGGCCC	802
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
Db	803	TGTGTGAGGTGAGCTACAAAGTCTGTTCTGGGTTCGAGTCTGAGCTGAGTCCAGAA	862
Qy	281	GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaAArgValSerAla	300
Db	863	GGAAATTACCTGCTGCTCTCCCTAAATTCCAGTGGGGCGGAGTGGCGAGGTTCGCT	922
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
Db	923	GTCAACGCCACAAGCTGGGAGCCTCTCACCAACCTCTCTTTGGTCTCTTGGATTACGCC	982
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
Db	983	TCTGCCCCCGTAGCGTGGCAGTCAAGCATCGTGGGAGCAGGAGCTACTGCTGACC	1042
Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaAArgAspGlyAsp	360
Db	1043	TGGCAACCGGGGCTGGGGAACCACTGGAGCATGTAGTGACCTGGGCTCCAGATGGGGAC	1102
Qy	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
Db	1103	CCCTGGAGAAACTCAACTGGGTCCGGCTTCCCTCCCTGGGAACCTCAGTGTCTGTTHACA	1162
Qy	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
Db	1163	GGAAATTTCACTCGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC	1222
Qy	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
Db	1223	TTGGCCTCTGCATCTCTCGCTCGGGGTTCAGGGAGAAATTAGCACCCCTAGTGGGGCCA	1282
Qy	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
Db	1283	ACGCTTTGGGCACTCCAGATGCCCCCTCCAGAGACCCCCCCCATAGCGTGGGAGAGGTC	1342
Qy	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
Db	1343	CCAAGGCACCGCTTCAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGAAC	1402
Qy	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
Db	1403	AGCCCTCTCGTCTGCATGAATGTGAGTGGCAACACACAGAGTGTCAACCTGCTGACCTT	1462
Qy	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
Db	1463	CCTTGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT	1522
Qy	501	GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly	520
Db	1523	GGTCCCATCTCGGCTTCATCTACACAGATAACACCTCAGGTGGAAGTTCTGCCGGGC	1582
Qy	521	IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
Db	1583	ATCCTATTCTGTGGGGCTTGTTCCTGTGGGGGTGTGGCCTGAGCCCTGGCCACCTCTGGA	1642
Qy	541	ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp	560
Db	1643	AGGTGCTTACCCTTAAGGCACAAAGTACTGCCCGCTGGGTCTGGGAGAAAGTTCTTGAT	1702
Qy	561	ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu	580
Db	1703	CCTGCCAACAGCAGTTCA-----	1720
Qy	581	GlyAspLeuProIleLeuGluGluMetGluProProValMetGluSerSer	600
Db	1720	-----	1720

QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1720 ----- 1720

QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1721 -----GGCCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 1756

RESULT 6
US-09-275-925-2
; Sequence 2, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..1759
US-09-275-925-2

Alignment Scores:
Pred. No.: 7,92e-243 Length: 2368
Score: 3150.00 Matches: 578
Percent Similarity: 90.88% Conservativeness: 0
Best Local Similarity: 90.88% Mismatches: 0
Query Match: 90.05% Indels: 58
DB: 3 Gaps: 1

US-10-088-950A-1 (1-636) x US-09-275-925-2 (1-2368)

QY 1 MetArgGlyValArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 23 ATGCGGGAGGAGGAGGCGCCCTTTCTGGCTGTGGCCGCTGCCAAGCTGGCGCTGCTG 82

QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 83 CCTCTGTTGGGTGCTTTTTCACGCGACGCGCTGCCAGGAGCGCCCGGCGACCTGACAG 142

QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60

Db 143 TGCTACGGAGTTGGACCTTGGCGACTTGAACCTGCTCGTGGAGCCTCTTGGGACCTG 202

QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80

Db 203 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAAGTACCCTGTCACAAAACCCAGACT 262

QY 81 ValAlaValAlaAlaGlyValArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100

Db 263 GTGGCAGTGGCAGCGCGAGCGAGCTGGTGGCCATTCTCTCGGAAACAGCTCACCATGTCT 322

QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120

Db 323 GACAAACTCTCTGTCTGGGCGACTAAGCGAGCGCCAGCTCTCTGCCCCCGCTCTCGTG 382

QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140

Db 383 AACCTAGAACCCAAATGAAGCCAAACGCCCCCGCTGGGCCCTGAGCTGACTTTTCC 442

QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160

Db 443 GAGGATGACCCCTGGAGGCCACTGTCTCATTTGGGCCCCCACCCTACATGCCCATTCTATAA 502

QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180

Db 503 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTGAGGAGCGGCGCTGACCCCTGCTGGAA 562

QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200

Db 563 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTAGATCCCAAGATTTGAGAGTAGCCACT 622

QY 201 GlyTyrLysValTyrGlyValArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220

Db 623 GGCTACAAAGTGTATGGCGCTGCGGATGAGAAAGAGAGGATTCTGGGGCGAGTGG 682

QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240

Db 683 AGCCCCATTTGTCTCTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 742

QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260

Db 743 AACCTCTGTGGAGCGCTGGAGGAGAGAACCTTTGCTTCTATGGAAGCCGCCAGGGGCC 802

QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280

Db 803 TGTGTGAGGTGAGCTACAAAGTCTGGTTCGGGTGGAGTCTGAGTCTGAGTCCAGAA 862

QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300

Db 863 GGAATTACCTGCTGCTCTCCCTAATTCCTAGTGGGGCGAGTGGGGCCAGGGTGTCCGCT 922

QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320

Db 923 GTCAACGCCCAAGCTGGAGCCCTCTACCAACCTCTCTTTGGTCTGCTTGGATTACGCC 982

QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340

Db 983 TCTGCCCCCGCTAGCGTGGAGTCAGCAGTCTGCTGGAGCAGCAGCTACTGTTGACC 1042

QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360

Db 1043 TGGCAACCGGGGCGCTGGGGAAACCACTGGAGCATGTAGTGGGCTCGAGATGGGAC 1102

QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380

Db 1103 CCCCTGGAGAAACTCACTGGTCCGGTTCCTCCCTGGGAACCTCAGTCTGTTACCA 1162

QY 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400

Db 1163 GGGAAATTTCACTGTCCGGGTCCCTTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1222

QY 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420

QY	234	LysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluProLeuLeu	253
Db	692	GAGCATGTGGTATCTCGGGACCGCTGTGAACCTTCGGCAAAACGGGCAGCCCTCCT	751
QY	254	LeuTrpLysAlaProGlyProCysValGlnValSerTyrlsValTrpPheTrpValGly	273
Db	752	GTCCTGGGAAGGACCACAAGACCTTGTCGAGGTACTTACACAGTCTGGTTGGGGCTGGA	811
QY	274	GlyArgGluLeuSerProGluGlyIleThrCysCysCysSerLeuIleProSerGlyAla	293
Db	812	GATATTACTACACTCAAGAAGAGGTCCCGTCTGCAAGTCCCCTGTCCCTGCATGATG	871
QY	294	GluTrpAlaArgValSerAlaValAsnAlaThrserTrpGluProLeuThrAsnLeuSer	313
Db	872	GAGTGGGCTGTGGTCTCTCTCGGCAACAGCACCAAGCTGGGTGCCCTCCCAACCACTGCT	931
QY	314	LeuValCysLeuAspSerAlaSerAlaProArgSerValalavalSerSerIleAlaGly	333
Db	932	CTGGTGTCTGGTCCAGAAATCTGCCCTCTGACCTGGGAGTGACGAGTGTGATGGG	991
QY	334	SerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGluHisValVal	353
Db	992	AGCCCCGGATAAAGGTGACCTGGAACACAGGACACAGGAACCATTTGGAGTATGTGGT	1051
QY	354	AspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProGly	373
Db	1052	GACTGGGCTCAAGATGTGTACAGCTGGCAAGCTCAACTGGAGCCCTCTCCCCCTCGGA	1111
QY	374	AsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrrArgIleThrVal	393
Db	1112	AACCTCAGCACATTGTTACCAAGGGAGCTCAAAGGAGGGGTACCTATCGAATTTACAGT	1171
QY	394	ThrAlaValSerAlaSerGlyLeuAlaSerAlaSerSerValTrpGlyPheArgGluGlu	413
Db	1172	ACTGCAGTACTCTCGAGGATTAAGTCTGCACCCCTCAGTTTGGGATTCAGAGAGAG	1231
QY	414	LeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPro	433
Db	1232	TTAGTACCCCTTGCTGGGCCAGCAGCTTTGGCGACTTCCAGATGACCCCCAGGGACACCT	1291
QY	434	AlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyThr	453
Db	1292	GTTGTACCCCTGGGAGAGTAGTACCAGACACAGCTCAGAGGCCAGGCTACTCATCACCC	1351
QY	454	LeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsnThrGln	473
Db	1352	TTCGCGATCAGAGCAGCAGGCCTCTCCACTGTCTGCAGGAACGTGACGATCAAACCCAG	1411
QY	474	SerValThrLeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThr	493
Db	1412	ACTGCCACTCTGCCCAACCTTCACTCGGGTTCTTCAAGCTGTGGGTGACGGTGTCCACC	1471
QY	494	IleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeu	513
Db	1472	GTTGCAGAGCAGGGGCCACCTGTGTCCGACCTTCACTTCACTTACCAGATAATAGGATC	1531
QY	514	ArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGly	533
Db	1532	AGGTGGAAAGCTCTGCCCTGGTTCTCTCCCTGTGGGGTTTGTCTTGATGGGGCTGGGC	1591
QY	534	LeuSerLeuAlaThrSer-----GlyArgCysTyrrHisLeuArgHisLysVal	549
Db	1592	CTGAGCCTGGCCGATACCGAGGTGCCTACAGGCCAGGTGCTTACACTGGCGACACAGTTG	1651
QY	550	LeuProArgTrpTrpTrpGluLysValProAspProAlaAsnSerSerGlyGlnPro	569
Db	1652	CTTCCCCAGTGGATCTGGGAGAGGGTTCCTGATCCTGCCAACAGCAATTTCTGGGCAACCT	1711
QY	570	HisMetGluGlnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGlu	589
Db	1712	TACATCAAGGAGGTGAGCCTGCCCAACCCGCCAAGGACGGACCATCTCTGGAGGTGGAG	1771
QY	590	GluMetGluProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu	609

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Db      1772 GAAGTGGAGCTACAGCCTGTTGTGGAGTCC-----CCTAAAGCCTCTGCCCGGATT 1826
      610 AspSerGlyTyrGluLysHisPheLeuProThrProGluGluLeuGlyLeuLeu 627
Db      1823 TACTCTGGGTATGAGAAACACTTCTCTGCCACACAGAGGAGCTGGGCCTTCTA 1876

RESULT 8
US-09-073-594-6
; Sequence 6, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..1882
US-09-073-594-6

Alignment Scores:
Pred. No.: 4,66e-154 Length: 2589
Score: 2044.00 Matches: 388
Percent Similarity: 72.65% Conservative: 61
Best Local Similarity: 62.78% Mismatches: 161
Query Match: 58.43% Indels: 8
DB: 2 Gaps: 3

US-10-088-950A-1 (1-636) x US-09-073-594-6 (1-2589)

Qy      14 LeuProLysLeuAlaLeuLeuProLeuLeuTrpValLeuPheGlnArgThrArgProGln 33
Db      35 CTCACCGCGTTGGAGCTTCTGCTGTCGCTGATGTCTGCGGACGCGGCCCCAC 94
Qy      34 GlySerAlaGlyProLeuGlnCysTyrGlyValGlyProLeuGlyAspLeuAenCysSer 53
Db      95 GGCAGTCTCAGGCCCATCTGCAGTGTCTACAGCTCGTCCCTCGGGAATCTGAACTGCTCC 154
Qy      54 TrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyr 73

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Db 155 TGGGAACCTTTGGGGGAGCTCCAGACTCCAGCTGTGCTGTATACACAGAGTCAGAAATAC 214
Qy 74 ArgSerAsnLysThrGlnThrValAlaValAlaAlaGlyArgSerTrpValAlaIlePro 93
Db 215 CATCCAATAGAGTCTGGGAGGTGAAGTCTTCCAAACAGAGTTGGTGACCATTCCTCC 274
Qy 94 ArgGluGlnLeuThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnPro 113
Db 275 CGGAACAGTTTCACCATGGCTGCACAACTCTCATCTGGGGGACACAAAGGAGCGCCT 334
Qy 114 LeuTrpProValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeu 133
Db 335 CTGTGGCTCTGTCTGTGAACCTGGAGACCCAAATGAAGCCAGACACACCTTCAGATC 394
Qy 134 GlyProAspValAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaPro 153
Db 395 TTCTCTCAAGTGGATATTTCTGAGGAAGCAACCTGGAGGCCACTGTGCAGTGGGCGCG 454
Qy 154 ProThrTrpProSerHisLysValLeuIleCysGlnPheHisTyrArgCysGlnGlu 173
Db 455 CCGGTGTGGCCACCGCAGAAAGCTCTCACCTGTCTCAGTTCCGGTACAAAGGAATGCCAGGCT 514
Qy 174 AlaAlaTrpThrLeuLeuGluProGluLeuLysThrIleProLeuThrProValGluIle 193
Db 515 GAAGCATGGACCCGGCTGGAGCCCGCAGCTGAAGACAGATGGGCTGACTCTCTGTGTGAGATG 574
Qy 194 GlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213
Db 575 CAGAACCTGGAACTGGCACCTGTACAGGTGTCTGGCCGCTGCCAGGTGGAGAACGGA 634
Qy 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaPro 233
Db 635 TATCCA--TGGGGCGAGTGGAGTTGCGCCCTGTCTCCAGACGCCATCTTAGATCTCT 691
Qy 234 LysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeu 253
Db 692 GAAGATGTGGGTATCGGGACCGCTCTGTGAACCTTCTGGCAACCGGCGAGCCCTGCTT 751
Qy 254 LeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTrpValGly 273
Db 752 GTCTGGAAGGACCAAGACCTTGTGTGAGTGACTTACACAGTCTGTGTTGGGGTGGGA 811
Qy 274 GlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuIleProSerGlyAla 293
Db 812 GATATTACTACACTCAAGAGAGGTCCGCTGCTGCAAGTCCCTGTCCCTGTCATGTATG 871
Qy 294 GluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAsnLeuSer 313
Db 872 GAGTGGGCTGGGTCTCTCTGGCAACAGCACCGAGCTGGGTGGCTCCCAACCACTGTCT 931
Qy 314 LeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerIleAlaGly 333
Db 932 CTGTGTGTCTGGCTCCAGATCTGCCCTGTGACGTGGGAGTGAGCAGTGTGTATGGG 991
Qy 334 SerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGluHisValVal 353
Db 992 AGCCGAGGATAAAGGTGACCTGGAACAAGGGACCCAGGAAACCATTTGGAGTATGTGTG 1051
Qy 354 AspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProGly 373
Db 1052 GACTGGGCTCAAGATGTGTGACAGTCTGGCAAGCTCAACTGGACCCCTCTCCCCCTGGA 1111
Qy 374 AsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVal 393
Db 1112 AACCTCAGCATTGTTACCAAGGGAGTTCAAGAGGGGGTACCTATCGANNTACAGTG 1171
Qy 394 ThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluGlu 413
Db 1172 ACTCAGTATACTCTGGAGGATTAGTGTCTGCACCTCAGTTTGGGATTTCAGAGAGGAG 1231
Qy 414 LeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPro 433
Db 1232 TTAGTACCCCTTGTGGGCCAGCAGTGTGGCGACTTCCAGATGTACCCCGGAGACACCT 1291

Qy 434 AlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrThr 453
Db 1292 GTTGTAGCTGGGAGAGTACCAAGACACACAGCTCAGAGCCAGGCTACTCTACTACACC 1351
Qy 454 LeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsnThrGln 473
Db 1352 TTCTGCATACAGACGAGAGCCCTCTCCACTGTCTGCAGGAACGTCGAGCAGTCAAACCCAG 1411
Qy 474 SerValThrLeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThr 493
Db 1412 ACTGCCACTCTGCCAACCTTCACTCGGGTTCCTCAAGCTGTGGGTGACGGTCTCCACC 1471
Qy 494 IleAlaGlyGlnGlyProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeu 513
Db 1472 GTTGCAGACAGGGCCACCTGGTCCCGACCTTTCACTTCACCTACACAGATAATAGGATC 1531
Qy 514 ArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGly 533
Db 1532 AGGTGGAAGCTCTGCCCTGTCTTCTGTCCTGGGGTTTGTCTTCTGATGGGCTGTGGC 1591
Qy 534 LeuSerLeuAlaThrSer-----GlyArgCysTyrHisLeuArgHisLysVal 549
Db 1592 CTGAGCTTGCCAGTACCAGTGCCTACAGCCAGGTGCTTACACTGGCCGACAAAGTTG 1651
Qy 550 LeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerSerGlyGlnPro 569
Db 1652 CTTCCCGAGTGGATCTGGGAGAGGGTCTCTGATCTCTGCCAACAGCAATCTCTGGCAACCT 1711
Qy 570 HisMetGluGlnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGlu 589
Db 1712 TACATCAAGAGGTGAGCTGCCCCAACCGCCCAAGACGAGCCCATCTCTGGAGTGGAG 1771
Qy 590 GluMetGluProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu 609
Db 1772 GAAGTGGAGTACAGCTGTGTGGAGTGC-----CTTAAGCTCTGCCCGGCTTCTA 1822
Qy 610 AspSerGlyTyrGluLysHisPheLeuProThrProGluLeuGlyLeuLeu 627
Db 1823 TACTCTGGGTATGAGAAACACTTCTCTGCCACACAGAGGAGCTGGGCTTCTA 1876

RESULT 9

US-09-275-925-6
; Sequence 6, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSES: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:

Db	752	GTCTGAGAGGCCCAAGACCTTGTGTGCAGGTGACTTACACAGTCTGTTTGGGCTGGA	811
Qy	274	GlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuLeuProSerGlyAla	293
Db	812	GATATTACTACAACCTCAAGAGAGGTCCCGTGTGCAAGTCCCGTGTCCCTGATGTGATG	871
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Db	872	GAGTGGGCTGTGTCTCTCTGTCACACAGCAGCAGCTGGGTGCTCCCAACACCTGTCT	931
Qy	314	LeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerIleAlaGly	333
Db	932	CTGGTGTCTTGCTCCAGNACTGCCCCCTGTGACGTGGAGTGAAGCAGTGTGTATGGG	991
Qy	334	SerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGluHisValVal	353
Db	992	AGCCCCAGGATTAAGGTGACCTCGAAACAAGGACGAGCAACCATTTGGAGTATGTGGT	1051
Qy	354	AspTrpAlaArgAspGlyAspProLeuGluLeuLeuAsnTrpValArgLeuProProGly	373
Db	1052	GACTGGGCTCAAGATGGTGAACCTGGACAGCTCACTGGACCCGTCTCCCCCTTGGGA	1111
Qy	374	AsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVal	393
Db	1112	AACTCTCAGCACATGTGTTACAGGGAGATTCAAAAGGAGGGGTACCCCTATCGAATTACAGT	1171
Qy	394	ThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluGlu	413
Db	1172	ACTGCAGTATACTCTCGAGGATTTAGCTGTCTGCCACCTCAGTTTGGGGATTTCAGAGGAG	1231
Qy	414	LeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPro	433
Db	1232	TTAGTACCCCTTGCTGGGCCAGCAGTTTGGCGACTTCCAGATGACCCCCCAGGGACACCT	1291
Qy	434	AlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrThr	453
Db	1292	GTGTGTAGCTGGGGAAAGTACCACAAGACACAGCTCAGAGCCAGGCTACTACTACACC	1351
Qy	454	LeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsnThrGln	473
Db	1352	TTCTGCATACAGACAGAGGCCCTCTCCACTGTCTGCAGGAACGTGAGCAGTCAAAACCCAG	1411
Qy	474	SerValThrLeuProAspLeuProTrpTrpGlyProCysGluLeuTrpValThrAlaSerThr	493
Db	1412	ACTGCCACTCTGCCAACCTTCACTCGGGTTCCTTCAAGCTGTGGGTGAGCGGTGTCCACC	1471
Qy	494	IleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeu	513
Db	1472	GTTCAGGACAGGGCCCACTGTGTCCGACTTTCACCTTCCACCTACAGATAATAGGATC	1531
Qy	514	ArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGly	533
Db	1532	AGGTGGAAGACTCTGCCCTGGTTTCTGTCCCTGTGGGTTTGTCTTCATGTGGGTGTGGC	1591
Qy	534	LeuSerLeuAlaThrSer-----GlyArgCysTyrHisLeuArgHisLeuVal	549
Db	1592	CTGAGCTGTGCCAGTACCAGGTGCCTACAGGCCAGGTGCTTACACTGGCGACACAGTTG	1651
Qy	550	LeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerSerGlyGlnPro	569
Db	1652	CTTCCCCAGTGGATCTGGGAGAGGTTCTTCGTATCTCTGCCAACAGCAATTTCTGGGCAACCT	1711
Qy	570	HisMetGluGlnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGlu	589
Db	1712	TACATCAAGAGGTGAGCTCTGCCCAACCCCAAGGACGACCATCTCTGGAGGTGGAG	1771
Qy	590	GluMetGluProProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu	609
Db	1772	GAAGTGGAGCTACAGCTGTGTGTGAGTCC-----CCTAAAGCCTCTCTGCCCGATT	1822
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Db 1823 TACTCTGGGTATGAGAAACACTTCTCTGCCCAACAGAGGAGCTGGGCCTTCTA 1876

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Db 2077 CAATGTCCTGCTCTGATTCAGAGAACATAAAATCCATCATCTGTTATGAATCCGTGT 2136
QY 393 lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluG1 413
Db 2137 GTATGCACTCTCAGGGGAT--CAAGGAGGATGCAGCTCCATCTGGGTAACTCTAAGCA 2193
QY 413 uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProGlyThrPr 433
Db 2194 CAAAGCACCATGAGTGGGCCCCACATTAATGCCATCACAGAG--GAAAAGGGGAGCAT 2250
QY 433 oAlaIleAlaTrpGlyValProArgHisGlnLeuArgGlyHisLeuThrHisTyrTh 453
Db 2251 TTTAATTTTATGAACAGCATTCATCCATCCAGAGCAATGGGCTGCTCTCCATATATAG 2310
QY 453 rLeuCys-----AlaGlnSerGlyThrSerProSerValCys-----MetAs 467
Db 2311 GATATACTGAAGGAACGGGACTCCAACTCCAGCGCTCAGCTCTGTGAATTCCTCTACAG 2370
QY 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
Db 2371 AGTCTCCCAAAATTCATCCATCAACACAGCCCTGCAG--CCCGAGTGACATATGTCTC 2427
QY 487 uTrpValThrAlaSerThrIleAlaGlyGlnGlyProGlyProIleLeuArgLeuHi 507
Db 2428 GTGATGACAGCTCTCAGAGCTGCTGTGTAAGATTCACCGGAATGAGAGGAATTTTG 2487
QY 507 sLeuProAspAsnThr-LeuArgTrpLysValLeuPro-----GlyIleLeuPheL 524
Db 2488 TCTGCAAGGTAAAGCCAAATGGATGGCTTTGTGGCACCACCAAGCATTTGCTATCAT 2547
QY 524 euTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrH 544
Db 2548 CATGGTGGGCATTT-----TCTCAACGCATTTACTTCCAGCAAAAGGTGTGTGT 2595
QY 544 iLeuArgHisLysValLeuProArgTrpValTrpGlyLysValProAspProAlaAsnS 564
Db 2596 T-CTCTAGACGCCCTCAGACCTCAGTGGTAGCAGAGAAATTCAGATCCAGCAAAATA 2654
QY 564 erSerSerGlyGlnProHis-----MetGluGlnValProGluAlaGlnP 579
Db 2655 GCACCTTGGCGTAAAGAAATATCCCATTCGACAGGAGAGACACAGCTGCCCCCTGGACAG 2714
QY 579 roLeuGlyAspLeuProIleLeuGluValGluGluMetGluProPro----- 595
Db 2715 TCCTGATAGACTGGCCCAACCCCTGAA-----GATCCTGAACCGCTGCTCATCA 2762
QY 596 -----ValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu----- 609
Db 2763 GTGAAGTCTTCA-TCAAGTGACCCCACTTTTCAGACATCCCCCTGCTCCAACTGGCCA 2821
QY 610 -----AspSerGlyTyr-GluLysHisPheLeuProThrPro 621
Db 2822 CAAAAGGAAAAAGGAATCCAAAGGTCTATCAGGCGCTCTGAGAAAGACATGATGCACAGTGC 2881
QY 622 GluGluLeuGlyLeuLeuGlyProProArgProGlnValLeu 635
Db 2882 TCA-----AGCCACCACCTTCCAAAGCTCTC 2908
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RESULT 11

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US-08-915-495-1
; Sequence 1, Application US/08915495
; Patent No. 5852176
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
```

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STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4040 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 641..3226
US-08-915-495-1
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Alignment Scores:

Pred. No.:	2,02e-20	Length:	4040
Score:	381.50	Matches:	189
Percent Similarity:	38.18%	Conservative:	92
Best Local Similarity:	25.68%	Mismatches:	285
Query Match:	10.91%	Indels:	172
DB:	2	Gaps:	35

US-10-088-950A-1 (1-636) x US-08-915-495-1 (1-4040)

QY	12	TrpProLeuProLysLeuAla-Leu-----LeuProLeuLeuTrpValLeuPhe-----	27
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QY	27	-----	27
Db	943	CAAACTGGCCTGTATCAATAGTGAATTCAAATATGTGGAGCAGAGATCTTCGTGG	1002
QY	28	-----GlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCysTyrGlyValGlyPr	46
Db	1003	TGTTGCTCTCAGAACACAGCCTCAAAAT-----TTATCTCGCATACAGAGGGAGA	1050
QY	46	oleuGlyAspLeuAsnCysSerTrpGluProLeuGlyAsp-----	59
Db	1051	ACAGGGAGACTGGCGCTGCACCTGGGAAAGAGGACGACACCCACTTATACATGAGTA	1110
QY	60	-----LeuGlyAlaProSerGluLeuHisLeuGlnSerGln-----	71
Db	1111	TACTCTACAGCTAAGTGGACCAAAAAATTTAACTGGCAGAGCAATGTAAAGACATTTA	1170
QY	72	-----LysTyrArgSerAsnLysTh	78
Db	1171	TTGTGACTATTGGACTTTGGAATCAACCTCACCCCTGAATCCTGAATCCAATTTTAC	1230
QY	78	rGlnThrVal---AlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLe	97
Db	1231	AGCCAAAGTTACTGCTGTCATAGTCTTGGAGAGCTCCTTTCACCTTCCA---TCCACATT	1287

Qy	97	uThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr	117
Db	1288	CACATCTTGTGACATAGTG	1320
Qy	117	oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspVa	137
Db	1321	GTGGGACATTAGATCAAAATTCAA--AAGGCTTCGTGAGCAGA	1363
Qy	137	lAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpPr	157
Db	1364	-----TGTAACCCTTTATTGGAGA-----GA	1383
Qy	157	oSerHisLysValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpTh	177
Db	1384	TGAGGGACTGTACTGCTTAATCCACTCAGATATCGGCCCCAGTAACACGAGGCTCTGGAA	1443
Qy	177	rLeuLeuGluProGluLeuLysThrIleProLeuThrProVal	193
Db	1444	TATG-----GTTAATGTTACAAGGCCAAAGGACACATGATTT	1482
Qy	193	eGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysG	213
Db	1483	GCTGGATCTGAACCAATTACAGAAATATGAATTTTCAGATTTCCCTTAAGCTACATCTTTA	1542
Qy	213	uGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPro	230
Db	1543	TAAGGGAAGTTGGAGTGATTTGGATGAATCATTTGAGAGCAAAACACCAAGAGAGGCC	1602
Qy	230	oSerAlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluG	250
Db	1603	TACTGGGATGTTAGATGCTCGGTACATGAACCGGCACATTGACTAC---AGTAGACAACA	1659
Qy	250	uProLeuLeuLeuTrpLys-----AlaProGlyProCysValGlnVa	264
Db	1660	GATTTCTCTTTCTCGGAAGAATCTGAGTGCTCAGAGGCAAGAGAAAATTTCTCCACTA	1719
Qy	264	lSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	282
Db	1720	TCAGGTGACCTTGCAGGAGCTGCAGAGGGAAGGCCATGACACAGAACATCATCAGAGCA	1779
Qy	282	eThrCysCysSerLeuIleProSerGlyAlaGluTrpAla---ArgValSerAlaVa	301
Db	1780	CACCTCTGGACCCACAGTCATTTCTAGAACCGGAATTTGGCTGTGCTGTCTGTGAGC	1839
Qy	301	lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe	319
Db	1840	AAATTTCAAAGGCAAGTTCTCTGCCCACTCGTATTTAAACATATGAACCTGTGTGAGGCAGG	1899
Qy	319	rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa	339
Db	1900	GTTCGTGGCTCTCGCCAGGTCTCTGCNAACTCA---GAGGGCATGGACAACATTTCTGGT	1956
Qy	339	lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl	356
Db	1957	GACTTGGCAGCTCCACGGAAGATCCCTCTGCTGTTTCAGGAGTACGTGGTGGAAATGGAG	2016
Qy	356	aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProG	373
Db	2017	AGAGCTCCATCCAGGGGGTGACACACAGGTCCTCTAAACTGGCTGAGGAGTCGACCTA	2076
Qy	373	yAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVa	393
Db	2077	CAATGTGTCTGTCTGATTTTCAGAGAACAATAAATCCTACATCTGTTTATGAATATCCGTGT	2136
Qy	393	lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerSerValTrpGlyPheArgGluG	413
Db	2137	GTATGCACTCTCAGGGGAT---CAAGGAGGATGCAGCTCCATCTCGGTAACTCTAAGCA	2193
Qy	413	uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr	433
Db	2194	CAAAAGCACCACTGATGTGGCCCCCACTAATATGCAATCATCAGAG---GAAAAGGGGAGCAT	2250

RESULT 12

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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/685,118
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Silverman, Robert A.
 REGISTRATION NUMBER: 35,682
 REFERENCE/DOCKET NUMBER: CD 9195
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-2863
 TELEFAX: (201) 235-2363
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4040 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 641..3226
 US-08-914-520-1

Alignment Scores:
 Pred. No.: 2,02e-20 Length: 4040
 Score: 381.50 Matches: 189
 Percent Similarity: 38.18% Conservative: 92
 Best Local Similarity: 25.68% Mismatches: 285
 Query Match: 10.91% Indels: 172
 DB: 2 Gaps: 35

US-10-088-950A-1 (1-636) x US-08-914-520-1 (1-4040)

QY 12 TrpProLeuProLysLeuAla-Leu-----LeuProLeuLeuTrpValLeuPhe----- 27
 Db 883 TGCCCACTCCCTCAATCTCAAGTCACAGCTCTCCCTTGGTACAACTTGTGTCTG 942
 QY 27 ----- 27
 Db 943 CAAACTGGCGCTGATCAATAGTGAATCAAAATGATGGAGCAGAGATCTTCCTGG 1002
 QY 28 ----GlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCysTyxGlyValGlyPr 46
 Db 1003 TGTTCCTCCAGACAGCTCAAAAT-----TTATCCTGCATACAGAGGAGGA 1050
 QY 46 oLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAsp----- 59
 Db 1051 ACAGGGGACTGTGGCTGCACCTGGGAAAGAGGACGAGACACCCACTTATACACTGAGTA 1110
 QY 60 -----LeuGlyAlaProSerGluLeuHisLeuGlnSerGln----- 71
 Db 1111 TACTCTACAGTAAGTGGACCAAAATTTTAACTGGCAGAACCAATGTAAGACATTTA 1170
 QY 72 -----LysTyxArgSerAsnLysTh 78
 Db 1171 TTGTGACTATTGGACTTTGGAATCAACCTCACCCCTGATCACTGAAATCCCAATTTTCA 1230
 QY 78 rGlnThrVal---AlaValAlaAlaGlyArgSerTrpValAlaAlaProArgGluGlnLe 97
 Db 1231 AGCCAAGGTACTGCTGCTCAATAGTCTTGGAGCTCTCTTCACTTCCA---TCCACATT 1287
 QY 97 uThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr 117
 Db 1288 CACATTTCTTGACATATG-----AGGCCTTT---CCTCC 1320
 QY 117 oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspVa 137
 Db 1321 GTGGGACATTAGATCAAAATTTCAA---AAGGCTTCGTCGAGCAGA----- 1363
 QY 137 lAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpPr 157
 Db 1364 -----TGTAACCTTTATTGGAGA-----GA 1383

QY 157 oSerHisLysValLeuIleCysGlnPheHisTyxArgCysGlnGluAlaAlaTrpTh 177
 Db 1384 TGAGGGAGCTGTACTGCTTAATCACTCACTAGATATCGCCCACTAACAGCAGGCTCTGAA 1443
 QY 177 rLeuLeuGluProGluLeuLysThrIleProLeuThrProVal-----GluI 193
 Db 1444 TATG-----GTTAATGTTTACAAAGGCCAAAGAACACATGATTT 1482
 QY 193 eGlnAspLeuGluLeuAlaThrGlyTyxLysValTyxGlyArgCysArgMetGluLysG 213
 Db 1483 GCTGGATCTGAACCATTTACAGAAATATGAATTTTCAGATTTCTCTTAACTTACATCTTTA 1542
 QY 213 uGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPro-----Pr 230
 Db 1543 TAAGGGAAGTTGGAGTGTGGAGTGAATCATTCAGAGACCAACACAGAGAGAGGCC 1602
 QY 230 oSerAlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGlu 250
 Db 1603 TACTGGGATGTAGATGTCTGTATGAAACGGCACATTCGACTAC---AGTAGACAACA 1659
 QY 250 uProLeuLeuLeuTrpLys-----AlaProGlyProCysValGlnVa 264
 Db 1660 GATTTCTCTTTCTGGAAGAAATCTGAGTGTCTCAGAGCAAGAGAAATTCCTCCACTA 1719
 QY 264 lSerTyxLysValTrpPheTrpValGlyGlyValGluLeuSerProGlu-----GlyI 282
 Db 1720 TCAGGTGACCTTGACAGGAGCTGACAGAGGGGAAAGCCATGACACAGAACATCACAGGACA 1779
 QY 282 eThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAla---ArgValSerAlaVa 301
 Db 1780 CACTCTCTGGACACAGTCATTCCTTAGAACCGGAAATTTGGGCTGTGGCTGTGTCTGCAGC 1839
 QY 301 lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe 319
 Db 1840 AAATTCAAAGGAGCTTCTCTGCCCACTGATTAACATAATGACCTGTGTGGGAGG 1899
 QY 319 rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa 339
 Db 1900 GTTGTGTGCTCTCTCGCAGGTCTCTGCAAACTCA---GAGGGCATGGACAACATTCGTGT 1956
 QY 339 lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl 356
 Db 1957 GACTTTGGCAGCTCTCCAGGAAAGATCCCTCTGCTGTTTCAGAGTACGTGGTGAATGAG 2016
 QY 356 aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProG 373
 Db 2017 AGAGTCTCATCCAGGGGTGGACACACAGGTCCCTCTAACTGGCTACGAGTCGACCCCTA 2076
 QY 373 yAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyxArgIleThrVa 393
 Db 2077 CAATGTGTCTGCTCTGATTTTCAGAGAACATAAAATCTTACATCTGTTATGAATCCGTGT 2136
 QY 393 lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluG 413
 Db 2137 GTATCACTCTCAGGGAT---CAAGGAGGATGACGCTCCATCTCTGGGTAACTTAAGCA 2193
 QY 413 uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr 433
 Db 2194 CAAAGCACCATCTAGTGGCCCCCACCACATTAATGCCATCACAGAG---GAAAGGGGAGCAT 2250
 QY 433 oAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyxTh 453
 Db 2251 TTTAATTTTCATGAACACAGCATTCAGTCCAGGAGCAAAATGGGCTCCCTCCTCATATAG 2310
 QY 453 rLeuCys-----AlaGlnSerGlyThrSerProSerValCys-----MetAs 467
 Db 2311 GATATCTGGAAGGAGGAGGAGGACTCCCACTCCAGGCTCAGCTCTGTGAAATTCCTACAG 2370
 QY 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
 Db 2371 AGTCTCCCAAAATTCACATCCAATAAACAGCCTGCAG---CCCCGAGTGACATATGTCTCT 2427

RESULT 14

US-07-923-976-3
Sequence 3, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2943 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 170..2677
US-07-923-976-3

Alignment Scores:
Pred. No.: 6,88e-14 Length: 2943
Score: 297.50 Matches: 173
Percent Similarity: 34.73% Conservative: 76
Best Local Similarity: 24.13% Mismatches: 289
Query Match: 8.50% Indels: 201
Gaps: 33

US-10-088-950A-1 (1-636) x US-07-923-976-3 (1-2943)

QY 50 LeuasnCysserTrpGluProLeuGlyAspLeuGlyAlapSerGlnLeuHisLeuGln 69
Db 587 CTCATCTGCCAGTGGGAGCCAGACCTTGACAGCCCAAGGGGACTCCCATCTCGACTGCCTGCTGAAG 646
QY 70 SerGlnLysTyArgSerAsn---LysThrGlnThrValalaVal----- 83
Db 647 AGTTTCAGAGCCGGGCAACTGTGACAGCCCAAGGGGACTCCCATCTCGACTGCCTGCTGAAG 706
QY 84 AlaalaGlyArgSerTrpValAlaIleProArgGlnGlnLeuThrMetSerApplysLeu 103
Db 84 AlaalaGlyArgSerTrpValAlaIleProArgGlnGlnLeuThrMetSerApplysLeu 103

319 rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa 339
1900 GTTGCTGGCTCTCGCCAGCTCTGCAAACTCA---GAGGCGATGACACAACTTCGT 1956
QY 339 lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl 356
Db 1957 GACTTGGCAGCTCCCGAGAAAGATCCCTCTGCTGTTTCAGGAGTAGCTGTGGTAATGGAG 2016
QY 356 aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProGl 373
Db 2017 AGAGCTCCATCCAGGGGGTGACACACAGAGTCCCTCTAACTGCGCTACGGAGTCCACCCTA 2076
QY 373 YAnLeuSerAlaLeuLeuProGlyAsnPhetrValGlyValProtyrArGilleThrVa 393
Db 2077 CATGTGTCTGCTCTGATTTCAGAGAACAATAAATCTTACATCTCTTATGAAATCCGTGT 2136
QY 393 lThralavalserAlaserGlyLeualaSerlaserValTrpGlyPheArgGluGl 413
Db 2137 GTATGCACTCTCAGGGGAT---CAAGAGGATGCGAGCTCCATCTGGGTAACTCTTAAGCA 2193
QY 413 uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr 433
Db 2194 CAAGCACCACTGAGTGGCCCCCACATTAATGCCATCAGAG---GAAAAGGGAGCAT 2250
QY 433 oAlaileAlatrpGlygluValProArgHisGlnLeuArgGlyHisLeuThrHisTyTh 453
Db 2251 TTAAATTCATGAACAGCATTCAGTCCAGGAGCAAAATGGGCTGCTCTCCCTCATATAG 2310
QY 453 rLeuCys-----AlaglnSerGlyThrSerProSerValCys-----MetAs 467
Db 2311 GATATCTGGAAGAGGAGGAGTCCAACCTCCAGCTCAGCTCTGTGAATTCCTACAG 2370
QY 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
Db 2371 AGTCTCCAAAATTCACATCCAATAAACAGCCTGCAG---CCCGAGTGACATATGTCCT 2427
QY 487 utrpvalThrAlaserThrilealaglyGlnGlyProProGlyProIleLeuArgLeuHi 507
Db 2428 GTGGATACAGCTCTGACAGCTCTGTGTGAAGATCCCAGGAAATGAGAGGGAATTTTG 2487
QY 507 sLeuProAspAsnThr-LeuArgtrpLysValLeuPro-----GlylleLeuPheL 524
Db 2488 TCTCAGAGTAAGCCAAATGGATGGTGTGGCCACCAAGCATTTGCATTGCTATCAT 2547
QY 524 euTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeualathrSerGlyArgCysTyRH 544
Db 2548 CATGTTGGGCAATTT-----TCTCAACACATTAATTCACAGCAAAAGGTGTTGT 2595
QY 544 iLeuArgHisLyseValLeuProArgTrpValTrpGluLysValProAspProAlaAsNs 564
Db 2596 T-CTCTAGAGCCCTCAGACCTCAGTGTGTAGCAGAGAAATTCAGATCCAGCAAATA 2654
QY 564 erSerSerGlyGlnProHis-----MetGluGlnValProGluAlaGlnP 579
Db 2655 GCATTTGGCTTAAGAAATATATCCATTCAGAGGAGGAGACACAGCTGCGCTTGGACAGCG 2714
QY 579 roLeuGlyAspLeuProIleleucluvallGluMetGluProProPo----- 595
Db 2715 TCCTGTATAGATGGCCCCAGCGCTGAA-----GATCTGTACCGCTGGTGCATCA 2762
QY 596 -----ValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu----- 609
Db 2763 GTGAAGTCTTCA-TCAAGTACCCCAAGTTTTCAGACATCCCGCTGCTCCAACTGGCCA 2821
QY 610 -----AspSerGlyTyR-glulysHisPheLeuProThrPro 621
Db 2822 CAAAGGGAAAAAGGAATCCAAGGTCAATCAGCGCTCTCAGAAAGACATGATGACAGTGGC 2881
QY 622 GluGluLeuGlyLeuLeuGlyProProArgProGlnValLeu 635
Db 2882 TCA-----AGCCCAACCTCCAAAGAGCTCTC 2908

Db 707 AAGGACGGGAGAGCCACCTGTCATCCACGCAACACCTGCTGTGTACCAAGATATG 766
Qy 104 LeuValTrp-----GlyThrIysAlaGlyGlnProLeuTrp--- 115
Db 767 GGCATCTGGGTGAGGAGAGATGCGCTGGGGACAGCATGTCCCAACACTGTGCTT 826
Qy 116 -----ProProValPheValAsnLeuLeuGlnMet 126
Db 827 GATCCCATGGATGTTGTGAACACTGGAGCCCGCCCATGCTGCGGACCATGGAGCCGCT 886
Qy 127 LysProAsnAlaProArgLeuGly-----ProAspValAspPhe 139
Db 887 GAAGGGCCCTCCCAAGAGAGGCTGCTCAGCTGTGCTGGAGCCA----- 934
Qy 140 SerGluAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHis 159
Db 935 -----TGGCAGCCAGGCGCTGCACATAAATCAG 961
Qy 160 LysValLeuIleCysGlnPhe-----HisTyrArgArgCysGlnGluAlaAlaTrpThrLeu 178
Db 962 AAG-----TGTGAGCTCGGCACAAAGCGCGAGCGTGGAGAAGCCAGCTGGGCACCTG 1012
Qy 179 LeuGluProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuLeu 198
Db 1013 GTGGGCCCC-----CTCCCTTGGAGGCGCTTCAGTATGAGCTC 1051
Qy 199 -----AlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213
Db 1052 TGGGGCTCTCCAGCCAGCGCTACACCTGCAGATACGCTGCATCCGCTGCCCTG 1111
Qy 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThr-ProProSerAlaPr 233
Db 1112 CCTGGCCACTGGAGCGACTGGAGCCCGCCAGCTGGAGTGAACACTACCGAAGCGGCCCC 1171
Qy 233 oLysAspValTrpValSerGlyAsnLeuCysGly-----ThrProGlyGlyGluGluPr 251
Db 1172 ACTCTCAGCTGGACACATGTTGGCGGAGGCGAGCTGGAGCCCGCCAGGA-----CAGTG 1225
Qy 251 oLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTr 271
Db 1226 -CAGCTGTTCTGGAG--CCAGTGGCCCTGGAGGAGACAGCGGAGTCCAGGTTA 1281
Qy 271 pValGlyGlyArgGluLeuSerProGlyIleThrCysCysSerLeuIleProse 291
Db 1282 TGTG-----GTTTCTTGGAGACCTC 1302
Qy 291 rGlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAs 311
Db 1303 AGGCCAGGCTGGGCGCCATCTGCCCTCTGCAACACACACAGAGCTCAGCTGCACCTTCCA 1362
Qy 311 nLeu-----SerLeuValCysLeuAspSerAla-----SerAl 322
Db 1363 CTGCTTTCAGAGCCAGGAGGTGGCGCTTGTGGCTATTAACCTCAGCCGGACCTCTCG 1422
Qy 322 aProArgSerValAlaValSerIleAlaGlySerThr----- 335
Db 1423 CCCCACCCGGTGTCTTCTCAGAAAGCAGAGGCGCCAGCTCTGACCAGACTCCATGCCAT 1482
Qy 336 -----GluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuG 350
Db 1483 GGCCCGAGACCTCAGACGCTCTGGGTAGGTGGAGCGGCCCGCCCAATCCATGGCCTCAGGG 1542
Qy 350 uHisValValAspTrpAlaArgAspGlyAspProLeuGluLysLeuAsn-----TrpVa 368
Db 1543 CTATGTATGATGATGGGCGCTGGGCGCCCGCCAGCGCGAGCAATAGCAAGACCTGGAG 1602
Qy 368 lArgLeuProProGlyAsnLeuSerAla---LeuLeuProGlyAsnPheThrValGlyVa 387
Db 1603 GATGAACAGAAATGGAGAGCCACGGGTGTTCTCTGAAGGAGAAATCAGGCCCTTTCA 1662
Qy 387 lProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSerAlaSerVa 407
Db 1663 GCTCTATGATCATCTGATCTCCCTTGTATACAGGACACCATCTGGGACCCCTCCAGCATG 1722

Qy 407 lTrpGlyPheArgGluGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAs 427
Db 1723 CTATGCTACTCTCAAGAAATGCTCTCCCTGAGCCAGAGCTG---CATCTAAAGCA 1779
Qy 427 pAlaProProGlyThrProAlaIleAlaTrpGlyValProArgHisGlnLeuArgL 447
Db 1780 CATTTGGAAGACCTGGGCACAGCTGGAGTGGTGGCTGAGCCCTCAGCTGGGGAAGAG 1839
Qy 447 yHisLeuThrHisTrpLeuCysAlaGlnSerGlyThrSerProSerValCysMetAs 467
Db 1840 CCCCCTTACCACCTACACCATCTTCTGGACCAAGCTCAGAACCAAGCTTCTCCGCCAT 1899
Qy 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
Db 1900 CTTGAATGCTCTCTCCCGTGGCTTGTCTCCATGGCTGGAG-----CCCGCCAGCTCT 1953
Qy 487 uTrp-----ValTh 490
Db 1954 GTATCATCATCCACCTCATGGCTGCAGCAGAGGTGGGGCCCAACCAAGTACAGTCTCAC 2013
Qy 490 rAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAs 510
Db 2014 CTGATGACCTTGACCCAGAGGGGTG-----GAGCTACACATC----- 2053
Qy 510 pAsnThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeu 530
Db 2054 -----ATCCTGGGCTGTTCGGCTCTCTGCTGTT 2082
Qy 530 u-----GlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArgHi 547
Db 2083 GCTCACCTGCTCTGTGGA-----ACTGCTGCTGTGTTCGAGCCCAACAG 2130
Qy 547 sLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerGl 567
Db 2131 GAAG-----AATCCCTCTGGCCAGTGTCTCCAGACCCAGCTCAGCAGCCTGGG 2181
Qy 567 Y-----GlnProHisMetGluGlnValPro-----GluAlaGl 578
Db 2182 CTCTGGGTGCCCAATCATGAGGAGGAGTGTCTTCAGCTGCCCGCTTGGCAGGCC 2241
Qy 578 nProLeuGlyAspLeuProIleLeuGluValGluGluMetGluProPro----- 595
Db 2242 ACCATCACCAGCTCAGAGTGTGGAGGAGTGAAGAAGCGGTGCTGGAGTC 2301
Qy 596 -----ValMetGluSe 599
Db 2302 CCATAACAGCTCAGAGACCTGTGGCTCCCTCCACTCTGGTCCAGACCTATGTCTCCAGGG 2361
Qy 599 rSerGlnProAlaGlnAlaThrAlaPro---LeuAspSerGlyTyrGluLysHisPheLe 618
Db 2362 GGACCCAGAGCAGTTTCCACCCAGCCCAATCCAGTCTGGCACCAGCATCAGTCTCT 2421
Qy 618 u-----ProThrProGluGluLeuGlyLeuLeuGlyPro----- 629
Db 2422 TTATGGCAGCTGTGGGAGAGCCCAAGCCAGGCGCCAGGCA-CTATCTCGCTGTG 2480
Qy 630 -----ProArgProGlnValLeu 635
Db 2481 ACTCCACTCAGCCCTCTTGGGGGCGCTCACCAGCCAGCCCAAGTCTCTA 2529

RESULT 15

US-09-023-655-1086

; Sequence 1086, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

ADDRESS: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1086:

SEQUENCE CHARACTERISTICS:

LENGTH: 2943 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g183046

US-09-023-655-1086

Alignment Scores:

Pred. No.: 6,88e-14 Length: 2943
Score: 297.50 Matches: 173
Percent Similarity: 34.73% Conservative: 76
Best Local Similarity: 24.13% Mismatches: 269
Query Match: 8.50% Indels: 201
DB: 4 Gaps: 33

US-10-088-950A-1 (1-636) x US-09-023-655-1086 (1-2943)

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QY 104 LeuValTrp-----GlyThrLysAlaGlyGlnProLeuTrp---115
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QY 116 -----ProValPheValAlaLeuLeuGluThrGlnMet 126
DB 827 GATCCCATGGATGTGTGAACCTGGAGCCCCCATGTGGGACCATGGAGCCGCT 886
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GenCore version 5.1.6
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Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	3498	100.0	2657	17	US-10-351-157-8	Sequence 8, Appli
3	3498	100.0	2657	17	US-10-352-554-8	Sequence 8, Appli
4	3498	100.0	2663	17	US-10-172-118-1092	Sequence 1092, Ap
5	3498	100.0	2663	17	US-10-342-887-1092	Sequence 1092, Ap
6	3498	100.0	3258	18	US-10-755-889-163	Sequence 163, App
7	3494	99.9	2628	10	US-09-791-497-13	Sequence 13, Appl
8	3494	99.9	2628	13	US-10-000-776-11	Sequence 11, Appl
9	3494	99.9	2628	18	US-10-777-790-11	Sequence 11, Appl
10	2044	58.4	2005	18	US-10-663-158-4	Sequence 4, Appli
11	381.5	10.9	4040	18	US-10-370-715B-67	Sequence 67, Appl
12	331	9.5	4023	17	US-10-398-666-11	Sequence 11, Appl
13	297.5	8.5	2943	17	US-10-641-643-1086	Sequence 1086, Ap
14	297.5	8.5	3139	16	US-10-252-157-457	Sequence 457, App
15	288.5	8.2	4026	17	US-10-351-157-134	Sequence 134, App
16	288.5	8.2	4026	17	US-10-352-554-119	Sequence 119, App
17	250	7.1	3085	15	US-10-177-293-229	Sequence 229, App
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19	250	7.1	3085	17	US-10-295-027-73	Sequence 73, Appl
20	250	7.1	3085	17	US-10-058-270A-31	Sequence 31, Appl
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22	250	7.1	3085	17	US-10-641-643-1131	Sequence 1131, Ap
23	250	7.1	3358	14	US-10-116-802-208	Sequence 208, App
24	250	7.1	7754	16	US-10-240-965-26	Sequence 26, Appl
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45	207	5.9	2402	10	US-09-892-949-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-663-158-3
; Sequence 3, Application US/10663158
; Publication No. US20040234522A1
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederic
; APPLICANT: Grewal, Iqbal
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: TYPE I CYTOKINE RECEPTOR TCOR
; FILE REFERENCE: 11669.123USC1
; CURRENT APPLICATION NUMBER: US/10/663,158
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 09/692,504
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,542
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (2433)..(2433)
; OTHER INFORMATION: n is a, c, t, or g
US-10-663-158-3

Alignment Scores:
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Score:          3498.00      Matches:      636
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
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US-10-088-950A-1 (1-636) x US-10-663-158-3 (1-2646)

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DB 1792 CTGCAACAGCAGTTTCAGGCCAGCCCAATGAGAGCAAGTACCTTGAGGCCCGAGCCCTT 1851

QY 581 GlyAspLeuProIleLeuGluValGluMetGluProProProValMetGluSerSer 600
DB 1852 GGGGACTTGGCCATCTCTGGAAGTGGAGGAGTGGAGCCCGCCGCTTATGGAGTCTCTCC 1911

QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
DB 1912 CAGCCCGCCAGGCCAGCCCGCTTCACTCTGGGTATGAGAACACTTCTCTGCCACA 1971

QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
DB 1972 CCTGAGGAGCTGGGCTTCTGGGGCCCCCGAGGCCACAGGTTCTGGCC 2019

```

RESULT 2

US-10-351-157-8
; Sequence 8, Application US/10351157
; Publication NO. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)...(2040)
US-10-351-157-8

Alignment Scores:

Pred. No.: 8 38e-310 Length: 2657
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-088-950A-1 (1-636) x US-10-351-157-8 (1-2657)

QY	1	MetArgGlyClyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
DB	133	ATGCGGGAGGCGAGGGCGCCCTTTCTGGCTGTGGCCGCTGCCAAGCTGGCGCTGCTG	192
QY	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
DB	193	CCCTGTGTGGGTGCTTTTCCAGCGACGCGTCCCGAGGCGCGCGGCGCCACTGCAG	252
QY	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
DB	253	TGCTACGGAGTTGGACCTTGGGGGACTTGAATCTGCTGTGGGAGGCTCTTGGGGACCTG	312
QY	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
DB	313	GGAGCCCCCTCCGAGTTACACCTCCAGAGCAAAAGTACCCTTCCAAACAAACCCAGACT	372
QY	81	ValAlaValAlaAlaGlyArgSerTrpValAlaAlaProArgGluGlnLeuThrMetSer	100
DB	373	GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCTCGGGAACAGCTCACCATGTCT	432
QY	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
DB	433	GACAACTCTTGTCTGGGGCACTAAGGCAAGCCGCTCTCTGGCCCCCGCTTCCTG	492
QY	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140

DB	493	AACCTAGAAACCCCAANTGAAGCCAAAGCCGCCCGGCTGGCGCTGACGTGGACTTTTTC	552
QY	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
DB	553	GAGGATGACCCCTCGGAGGCCACTGTCCATTGGGCCCCACTACATGGCCATCTCATAA	612
QY	161	ValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
DB	613	GTTCGTGATCTGCCAGTTCCACTACCGAAGATGTCCAGAGCGCGCTGGACCCCTGCGAA	672
QY	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
DB	673	CCGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAGATTTGGAGCTAGCCACT	732
QY	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
DB	733	GGGTACANAGTGTATGGCCGCTGCCGGATGGAGAGAGAGATTTGTGGGGCGAGTGG	792
QY	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
DB	793	AGCCCATTTTGTCTTCCAGACACCCCTTCTGCTCCAAAGATGTGTGGGTATCAGGG	852
QY	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
DB	853	AACCTCTGGGGACGCTGGAGGAGGAACTTGTCTTATGGGAAGGCCCCAGGGGCC	912
QY	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
DB	913	TGTGTGACAGTGAGCTCAAAAGTCTGGTCTGGGTTGGAGTCTGTGAGCTGAGTCCAGAA	972
QY	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
DB	973	GGAAATTACCTGTCTGCTCCCTAAATTCACAGTGGGGCGGAGTGGCGACGGGTCCGCT	1032
QY	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
DB	1033	GTCAACGCCACAGCTGGGAGCCCTCTCACCAACCTCTCTTGTGCTGCTTGGATTACGCC	1092
QY	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
DB	1093	TCGTGCCCCCGTAGCTGGAGTCCAGCATGCTGGGAGCAGGAGCTACTTGTGTACC	1152
QY	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
DB	1153	TGGCAACCGGGGCTGGGGAACCACTGGAGCATGTAGTGACTGGGCTCGAGATGGGAC	1212
QY	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
DB	1213	CCCTGGAGAAATCAACTGGGTCCGGCTTCCCGCTGGGAACCTCAGTGTCTGTACCA	1272
QY	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
DB	1273	GGGAATTCACATGTGCGGGTCCCTATCGAATCACTGTGACCGCATCTCTGTCTCAGGC	1332
QY	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
DB	1333	TTGGCCCTGTCATCTCCCTCTGGGGGTTCCAGGAGGAATAGCACCCCTAGTGGGGCCA	1392
QY	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
DB	1393	ACGCTTTGGCGACTCCCAAGATGCCCTCCAGGGAGCCCGCCCATAGCTGGGGAGAGGTC	1452
QY	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
DB	1453	CAAAGCACACAGCTTCAGGGCCACCTCACCCACTACACCTTGTGTGACAGAGTGGAAAC	1512
QY	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
DB	1513	AGCCCCCTCGTCTGCATGAATGTAGTGGCAACACACACAGAGTGTACCCTGCCTGACCTT	1572
QY	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
DB	1573	CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGAGAGGGCCCTCT	1632

QY 501 GlyProIleLeuArgLeuHisLeuProAspLeuThrLeuArgTrpLysValLeuProGly 520
 Db 1633 GGTCCCATCTCCGGCTTCATCTACAGATAACACCTTGAGTGGAAAGTTCTGCCAGGC 1692
 QY 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
 Db 1693 ATCCATATTCTGTGGGGCTGTCTCTGTGGGGTGTGGCCCTGAGCTGGCCACCTCTCGA 1752
 QY 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
 Db 1753 AGTGCTACCACTTAAGGCACAAAGTGTGCCCGCTGGGTCCTGGAGAAAAGTTCTCGAT 1812
 QY 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
 Db 1813 CTTGCCAACAGCAGTTCAGGCCAGCCACACATGGAGCAAGTACCTGAGGCCAGCCCTT 1872
 QY 581 GlyAspLeuProIleLeuGluValGluMetGluProProProValMetGluSerSer 600
 Db 1873 GGGGACTTGGCCCATCTGGAAGTGGAGAGATGGAGCCCCCGCGTTATGGAGTCTCTCC 1932
 QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
 Db 1933 CAGCCCGCCAGCCACCGCCCGCTTGACTCTGGGTATGAGAAGCACTTCTGCGCCACA 1992
 QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
 Db 1993 CCTGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2040

RESULT 3

US-10-352-554-8
 ; Sequence 8, Application US/10352554
 ; Publication No. US20030224487A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Kuiper, Joseph L.
 ; APPLICANT: Dasovich, Maria M.
 ; APPLICANT: Grant, Francis J.
 ; APPLICANT: Hammond, Angela K.
 ; APPLICANT: Novak, Julia E.
 ; APPLICANT: Gross, Jane A.
 ; APPLICANT: Dillon, Stacey R.
 ; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
 ; FILE REFERENCE: 02-01
 ; CURRENT APPLICATION NUMBER: US/10/352,554
 ; CURRENT FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: US 60/350,325
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/375,323
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/435,315
 ; PRIOR FILING DATE: 2002-12-19
 ; NUMBER OF SEQ ID NOS: 168
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 2657
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (133)...(2040)
 US-10-352-554-8

Alignment Scores:
 Pred. No.: 8,386-310 Length: 2657
 Score: 3498.00 Matches: 636
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-10-088-950A-1 (1-636) x US-10-352-554-8 (1-2657)

QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
 Db 133 ATGGGGAGGAGGAGGGGGCCCCCTTCTGGCTGTGGCGCTGCCCAAGCTGGCGCTGCTG 192
 QY 21 ProLeuLeuTrpValLeuPheGlnArgTrpArgProGlnGlySerAlaGlyProLeuGln 40
 Db 193 CCTCTGTGTGGGTGCTTTTCCAGCGGACGCTGCCCGAGGCGAGCGCGGCGGCGGCTCAG 252
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 Db 253 TGCTACGGAGTGGACCTTGGGCGACTTGAACCTGCTCGTGGGAGCCTCTTGGGAGACTG 312
 QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
 Db 313 GGAGCCCTCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCACAAACAAACCCAGACT 372
 QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 Db 373 GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCAGTGTCT 432
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120
 Db 433 GACAACTCTCTGTGGGCACTAAAGCAGGCGCAGCCTCTCTGGCCCCCGCTTCTGTG 492
 QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
 Db 493 AACCTAGAACCCAAATGAAGCCAAACGCCCGCTGGGCGCTGACGTGACTTTTCC 552
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 Db 553 GAGGATGACCCCTGGAGGCACCTGTCCATTGGGCCCCCACCCTACATGGCCATCTCATAAA 612
 QY 161 ValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 Db 613 GTTCTGATCTGCCAGTCTCCACTACCAAGATGTCCAGAGGCGGCTGGACCTCTGCTGAA 672
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
 Db 673 CCGGAGCTGAAGACCATACCCCTGACCCCTTTCAGATCCCAAGATTGGAGCTAGCCACT 732
 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluLeuAspLeuTrpGlyGluTrp 220
 Db 733 GGCTACAAAGTGTATGGCGCTGCGGATGAGAAAGAGGATTTGTGGGGCGAGTGG 792
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
 Db 793 AGCCCCATTTTGTCTTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 852
 QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPro 260
 Db 853 AACCTCTGTGGGACGCTGGAGGAGAGAACCTTTGCTTCTATGGAAGGCCCGGAGGCC 912
 QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
 Db 913 TGTGTGACAGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTGTGAGCTGAGTCCAGAA 972
 QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
 Db 973 GGAATTACTGCTGCTGCTCTCCCTAAATCCAGTGGGCGGAGTGGGCCAGGGTGTCCCT 1032
 QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
 Db 1033 GTCACGCGCACAAAGCTGGGAGCCTCTCACCAACCTCTCTTTGGTGTGCTTGGATTTCAGCC 1092
 QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
 Db 1093 TCTGCCCCCGGTAGGCTGGCAGTACAGCAGATCGCTGGAGCAGCAGGAGCTACTGTGACC 1152
 QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
 Db 1153 TGGCAACCGGGGCTGGGGNACCACCTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1212
 QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380

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Db 1213 CCCCTGGAGAACCACTCGGCTTCCCCCTGGGAACCTCAGTGTCTGTACCA 1272
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db 1273 GGGAAATTCACGTGTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1332
Qy 401 LeuAlaSerAlaSerSerValTrrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1333 TTGGCCTCTGCATCTCCGTCTGGGGTTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA 1392
Qy 421 ThrLeuTrrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrrpGlyGluVal 440
Db 1393 ACGCTTTGGGCACATCCAAAGATGCCCTCCAGGACCCCGCCATAGCGTGGGGAGAGGTC 1452
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTrrpThrLeuCysAlaGlnSerGlyThr 460
Db 1453 CCAGGCACCAAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGATGGAAACC 1512
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1513 AGCCCTCCGCTCGATGATGTGAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT 1572
Qy 481 ProTrrpGlyProCysGluLeuTrrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1573 CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCCT 1632
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrrpLysValLeuProGly 520
Db 1633 GGTCCTCATCTCCCGCTTCATCTACAGATACACCTCGAGGTGGAAAGTTCTGCCAGGC 1692
Qy 521 IleLeuPheLeuTrrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1693 ATCTATTCTTGTGGGCTTGTCTCTGTGGGTGTGGCCTGACCTGGCCACCTCTGGA 1752
Qy 541 ArgCysTrrpHisLeuArgHisLysValLeuProArgTrrpValTrrpGluLysValProAsp 560
Db 1753 AGGTGCTACCACTTAAGGCACAAAGTGTGCCCGCTGGGTCTGGGAGAAAGTTCTCGAT 1812
Qy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1813 CCTGCCAACAGCATTTAGGCCACCCACATGAGCAAGTACTGTAGGGCCACGCCCTT 1872
Qy 581 GlyAspLeuProfileLeuGluValGluMetGluProProProValMetGluSerSer 600
Db 1873 GGGGACTTGCCATCTCTGGAAGTGGAGAGATGGAGCCCGCCGCGTATTAGAGTCTCTCC 1932
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTrrpGluLysHisPheLeuProThr 620
Db 1933 CAGCCCGCCAGGCCACCGCCCGCTTGACTCTGGGTATGAGAGCACTTCTCTGCCCA 1992
Qy 621 ProGluLeuLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1993 CCTGAGAGCTGGGCCCTTCTGGGGCCCCCCCCAGGCCACAGGTTCTGGCC 2040
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RESULT 4

US-10-172-118-1092

; Sequence 1092, Application US/10172118

; Publication No. US20030224374A1

; GENERAL INFORMATION:

; APPLICANT: Dai, Hongyue

; APPLICANT: He, Yudong

; APPLICANT: Linsley, Peter

; APPLICANT: Mao, Mao

; APPLICANT: Roberts, Chris

; APPLICANT: Van 't Veer, Laura

; APPLICANT: Van de Vijver, Marc

; APPLICANT: Bernards, Rene

; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

; FILE REFERENCE: 9301-175-999

; CURRENT APPLICATION NUMBER: US/10/172.118

; CURRENT FILING DATE: 2002-06-14

; PRIOR APPLICATION NUMBER: 60/380,770

; PRIOR FILING DATE: 2002-05-14

; NUMBER OF SEQ ID NOS: 2699

; SEQ ID NO 1092

; LENGTH: 2663

; TYPE: DNA

; ORGANISM: Homo sapiens

; PUBLICATION INFORMATION:

; DATABASE accession NUMBER: NM_004843

; DATABASE ENTRY DATE: 2001-06-18

US-10-172-118-1092

Alignment Scores:

Pred. No.:	8,41e-310	Length:	2663
Score:	3498.00	Matches:	636
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-10-088-950A-1 (1-636) x US-10-172-118-1092 (1-2663)

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Qy 1 MetArgGlyGlyValArgGlyAlaProPheTrrpProLeuProLysLeuAlaLeuLeu 20
Db 139 ATGGGGGAGGCGAGGGCGCCCTTCTGGCTGTGGCCGCTGCCAAAGCTGGCGCTGCTG 198
Qy 21 ProLeuLeuTrrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 199 CCTCTGTGTGGGTGCTTTTCCAGGGAGCGGTCCCCAGGGCAGCGCGGGCCACTGCAG 258
Qy 41 CysTrrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrrpGluProLeuGlyAspLeu 60
Db 259 TGCTACGAGTGGACCCCTTGGGCGCACTTGAACCTGCTGTGGGAGCCTCTTGGGGACCTG 318
Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTrrpArgSerAsnLysThrGlnThr 80
Db 319 GAGAGCCCCCTCCAGGTGTACACCTCCAGAGCCAAAGTACCCTTCCAAACAAACCCAGACT 378
Qy 81 ValAlaValAlaAlaGlyArgSerTrrpValAlaIleProArgGluGlnLeuThrMetSer 100
Db 379 GTGGCAGTGGCAGCCGAGCGAGCTGGGTGGCCATTCTCGGGNACAGCTCACCATGTCT 438
Qy 101 AspLysLeuLeuValTrrpGlyThrLysAlaGlyGlnProLeuTrrpProValPheVal 120
Db 439 GACAAACTCTCTCTGGGGCACTAAGGCAGGCGAGCCTCTCTGGCCCCCGCTCTTCGTG 498
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db 499 AACCTAGAAACCCAAATGAAGCCAAACGCCCCCGCTGGGCGCTGACGTGGACTTTTCC 558
Qy 141 GluAspAspProLeuGluAlaThrValHisTrrpAlaProProThrTrrpProSerHisLys 160
Db 559 GAGGATGACCCCTGGAGGCCACTTCCATTTGGGCCCACTACATGGCCCATCTCATATA 618
Qy 161 ValLeuIleCysGlnPheHisTrrpArgCysGlnGlnAlaIleAlaTrrpThrLeuLeuGlu 180
Db 619 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTCCAGAGCGCGCTGAGCCCTGCTGAA 678
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
Db 679 CCGGAGCTGAAGACCATACCCCTGAGCCCTGTTGAGATCCAAAGATTTGGAGTAGCCACT 738
Qy 201 GlyTrrpLysValTrrpGlyArgCysArgMetGluLysGluLeuAspLeuTrrpGlyGluTrrp 220
Db 739 GGCTACAAAGTGTATGGCCGCTCCCGATGGAGAAAGAGAGATTTGTGGGGGAGTGG 798
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrrpValSerGly 240
Db 799 AGCCCATTTTGTCTTCCAGACACCGCCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 858
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrrpLysAlaProGlyPro 260
Db 859 AACCTCTGTGGGACGCTGGAGGAGGAGAACCTTTGCTTCTATGGAAGGCCCCAGGCCCC 918
```


Db 559 GAGGATGACCCCTGGAGGCCACCTGTCCATTGGGGCCCCCACCCTACATGAGCCCATCTCAFAA 618
Qy 161 ValLeuileCysGlnPheHisTyArgArgCysGlnGlnAlaAlaTTrpThrLeuLeuGlu 180
Db 619 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTGAGGAGGGGGCTGGACCCCTGCTGGAA 678
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
Db 679 CCGAGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAGATTTGGAGCTAGCCACT 738
Qy 201 GlyTyRlyValTyRlyArgCysArgMetGluLysGluLysGluLysGluLysGluLys 220
Db 739 GGCTACAAAGTGTATGGCGCTGCGGATGAGAGAAAGAGGATTTGTGGGGCGAGTGG 798
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTTrpValSerGly 240
Db 799 AGCCCCATTTTGTCTTCCAGACACCCGCTTCTGCTCCMAAAGATGTGGGTATCAGGG 858
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuThrLysAlaProGlyPro 260
Db 859 AACCTCTGTGGAGCGCTGGAGGAGAGAACCTTTGCTTCTATGGAAGGCCCCAGGGGCC 918
Qy 261 CysValGlnValSerTyRlyValTTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280
Db 919 TGTGTGAGGTGAGCTACAAAGTCTGGTTCGTGGGTGGAGTCTGTGAGCTGAGTCCAGAA 978
Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTTrpAlaArgValSerAla 300
Db 979 GGATTAACCTGCTGCTGCTCCCTAATTCCTAGTGGGGGGAGTGGGCCAGGGTTCGCT 1038
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
Db 1039 GTCAACGCCCAAGCTGGAGCCTCTCAACAACTCTCTTGGTCTGCTGGATTCAGCC 1098
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
Db 1099 TCTCCCCCGGTACGGTGGCAGTCAGCAGCATCTCGTGGAGCAGCGAGCTACTGGTGACC 1158
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTTrpAlaArgAspGlyAsp 360
Db 1159 TGGCAACGGGGCTTGGGAAACCACTGGAGCATGTAGTGACTGGGTTCGAGATGGGGAC 1218
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
Db 1219 CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCTCGGAACCTCAGTGTCTGTATACCA 1278
Qy 381 GlyAsnPheThrValGlyValProTyRArgIleThrValThrAlaValSerAlaSerGly 400
Db 1279 GGGAAATTTCACTGTCGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGTCTCAGGC 1338
Qy 401 LeuAlaSerAlaSerSerValTTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1339 TTGGCTCTGCATCTCTCGTCTGGGGTTTCAAGGAGAAATAGCACCCCTAGTGGGGCCA 1398
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTTrpGlyGluVal 440
Db 1399 ACGTTTGGGACTCCAAAGATGCCCTCCAGGAGCCCGCCATAGCTGGGGAGAGGTC 1458
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyRThrLeuCysAlaGlnSerGlyThr 460
Db 1459 CCAAGGACACCAAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGAACC 1518
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1519 AGCCCTTCCTGTCATGAATGTAGTGGGAACACACAGAGTGTACCCCTGCCTGACCTT 1578
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1579 CTTGGGGTCCCTGTGAGCTGTGGTGACAGCACTACCATCGTGTGACAGGGCCCTCT 1638
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1639 GGTCCCATCTCCGGCTTCATCTACCAAGATAACACCCCTGAGGTGGAAGTTCCTGCCAGGC 1698

RESULT 6

US-10-755-889-163

; Sequence 163, Application US/107555889

; Publication No. US20040171823A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB

; TITLE OF INVENTION: PATHWAY

; FILE REFERENCES: D0284 NP

; CURRENT APPLICATION NUMBER: US/10/755,889

; CURRENT FILING DATE: 2004-01-13

; PRIOR APPLICATION NUMBER: U.S. 60/440,068

; PRIOR FILING DATE: 2003-01-14

; PRIOR APPLICATION NUMBER: U.S. 60/469,757

; PRIOR FILING DATE: 2003-05-12

; NUMBER OF SEQ ID NOS: 823

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 163

; LENGTH: 3258

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-755-889-163

Alignment Scores:

Pred. No.:	1,07e-309	Length:	3258
Score:	3498.00	Matches:	636
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-10-088-950A-1 (1-636) x US-10-755-889-163 (1-3258)

Qy 1 MetArgGlyClyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20

Db 424 ATCGGGGAGGAGCGGGCGCCCTTTCTGGCTGTGGCGCTGGCCAAAGCTGGGGCTGCTG 483

Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40

Db 484 CCTCTGTGTGGGTGTCTTTTCCAGCGGACGCGTCCCGAGGCGCGCGGCGCCACTGCAG 543

Qy 41 CysTyRTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60

Db 544 TGCTACGGAGTTGACCCCTTGGCGGACTTGAACCTGCTCGTGGGAGGCTCTTGGGGACTG 603

Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyRArgSerAsnLysThrGlnThr 80

Db 604 GGAGCCCTCCCGCTTCACTCCAGAGCCAAAGATACCGTTCCAAACAAACCCAGACT 663

QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 Db 664 GTGGCAGTGGCAGCGGAGCTGGTGGCCATCTCTCGGACAGCTCACCATGCT 723
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
 Db 724 GACAAACTCTTGTCTGGGGCACTAAGGCAGCGCAGCCTCTCTGGCCCCCGCTCTCGTG 783
 QY 121 AsnLeuGluThrClnMetLysProAlaProArgLeuGlyProAspValAspPheSer 140
 Db 784 AACCTAGAAACCAATGAAGCAACACGCCCGGCTGGGCGCTGACGTGGACTTTTCC 843
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 Db 844 GAGGTGACCCCTGGAGGCCACTGTCCATTTGGGCCCACTACATGGCCATCTCATAA 903
 QY 161 ValLeuLeuCyGlnPheHisTrpArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 Db 904 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTACGAGGCGGCTGGACCTGTGGAA 963
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluAlaThr 200
 Db 964 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAAGATTTGGAGCTAGCCACT 1023
 QY 201 GlyTrpLysValTrpGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
 Db 1024 GGTACAAAGTGTATGGCGCTGCCGATGGAGAAAGAGGATTTGTGGGGCGAGTGG 1083
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
 Db 1084 AGCCCATTTTGTCTTCCAGACACCGCTTCTGCTCCAAAGATGTGTGGGTATCAGGG 1143
 QY 241 AsnLeuCyGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPro 260
 Db 1144 AACCTCTGTGGAGCGCTGGAGAGAGAACCTTCTGCTTCTATGGAAGGCCCGAGGCC 1203
 QY 261 CysValGlnValSerTrpLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
 Db 1204 TGTGTCCAGTGTGCTACAAAGTCTGGTCTGGTGGAGTCTGTGAGTGTGAGTCCAGAA 1263
 QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
 Db 1264 GGAATTAACCTGTCTGCTCCCTAAATCCAGTGGGGCGAGTGGGCCAGGCTGTCCGCT 1323
 QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
 Db 1324 GTCAACGCCACAGCTGGAGGCTCTCACCAACCTCTCTTGTGTCTGTGTGATTCAGCC 1383
 QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
 Db 1384 TCTGCCCGCTAGCTGGCAGTACAGCAGCATCGCTGGGACGAGCTACTGTGTGACC 1443
 QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
 Db 1444 TGGCAACCGGGGCTGGGCAACACCTGGAGCATGTAGTGGCTGGGCTCGAGATGGGAC 1503
 QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
 Db 1504 CCCCTGGAGAACTCAACTGGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGTGTACCA 1563
 QY 381 GlyAsnPheThrValGlyValProTrpArgIleThrValThrAlaValSerAlaSerGly 400
 Db 1564 GGGAAATTCATGTGGGGTCCCTATCGAATACATGTGACCGCATCTCTGTCTCAGGC 1623
 QY 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
 Db 1624 TTGGCTCTGCATCTCTGGGGTTCAGGAGGAATAGCACCCCTAGTGGGGCCA 1683
 QY 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
 Db 1684 ACCTTTTGGCAGTCCAAAGATGCCCTCCAGGGACCCCGCCATAGCGTGGGAGAGGTC 1743

QY 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTrpThrLeuCyAlaGlnSerGlyThr 460
 Db 1744 CCAAGGCACAGCTTCGAGGGCCACCTCACCCACATACACTTGTGTGCAACAGAGTGGAAACC 1803
 QY 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
 Db 1804 AGCCCTCCCGTGTGATGAATGTAGTGGCAACACACAGAGGTGCACCTGTGCTGACCTT 1863
 QY 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
 Db 1864 CTTTGGGTCTCTGTGAGCTGTGGGTGACAGCATCTACATCGCTGGACAGGGCCCTCTCT 1923
 QY 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
 Db 1924 GGTCCCATCTCCGGCTTCTATCTACAGATAACACCTGAGGTGAAAGTTCTGCGGGC 1983
 QY 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
 Db 1984 ATCTTATTTCTTGTGGGGCTTGTCTGTGGGGTGTGGCTGAGCCTGGCCACCTCTCTGA 2043
 QY 541 ArgCysTrpHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
 Db 2044 AGTCTCTACCACTTAAGGACCAAGTGTGCCCCCTGGGTCTGGGAGAAAGTTCTGTAT 2103
 QY 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
 Db 2104 CTTGCCAAACAGCAGTTTCAGGCCAGCCCCACATGGAGCAAGTACCTGAGGCCAGCCCTT 2163
 QY 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600
 Db 2164 GGGGACTTGGCCATCTCGAAGTGGAGAGATGGAGCCCCCGCGGTATGGAGTCTCTCC 2223
 QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTrpGluLysHisPheLeuProThr 620
 Db 2224 CAGCCCCCGCCAGGCCACCGCCGCTTGCATCTGGGTATGAGAGCATTCTCTGCCCCA 2283
 QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
 Db 2284 CTTGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2331

RESULT 7
 US-09-791-497-13
 ; Sequence 13, Application US/09791497
 ; Publication No. US20030008343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Kastelein, Robert A.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Pflanz, Stefan
 ; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
 ; FILE REFERENCE: DX010402
 ; CURRENT APPLICATION NUMBER: US/09/791,497
 ; CURRENT FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: 09/627,897
 ; PRIOR FILING DATE: 2000-07-27
 ; PRIOR APPLICATION NUMBER: 60/146,581
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 60/147,763
 ; PRIOR FILING DATE: 1999-08-06
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 2628
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (112) .. (2022)
 US-09-791-497-13

Alignment Scores: 1,92e-309 Length: 2628
 Pred. No.: 3494.00 Matches: 635
 Score:

Percent Similarity:	99.84%	Conservative:	0
Best Local Similarity:	99.84%	Mismatches:	1
Query Match:	99.89%	Indels:	0
DB:	10	Gaps:	0
US-10-088-950A-1 (1-636) x US-09-791-497-13 (1-2628)			
Qy	1	MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
Db	112	ATGGGGGAGGAGGGGGCGGCTTCTTGGCTGTGGCGCTGCCCAAGCTGGCGCTGCTG	171
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
Db	172	CCTCTGTGTGGGTGCTTTTCCAGCGGACGGCTCCCGAGGGCAGCGCGGGCCACTGCAG	231
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	232	TGCTACGGAGTTGACCCCTGGGGCAGCTTGAACTGCTCGTGGGAGCCTCTTGGGGAGCTG	291
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	292	GGAGCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	351
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	352	GTGCAGGTGGCAGCGGACGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGCT	411
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
Db	412	GACAACTCTTGTCTGGGGCAGTACGAGCGCCAGCCTCTCTGGCCCCCGCTTCTCGTG	471
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	472	AACCTAGAAACCCAAATGAAGCCAAACGCCCGCTGGGCGCTGACGTGGACTTTTCC	531
Qy	141	GluAspLeuProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	532	GAGGATGACCCCTGGAGGCGCAGTGTCTCATTTGGGCGCCACCTACATGGCCATCTCATAA	591
Qy	161	ValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
Db	592	GTTCTGATCTGCCAGTTCCACTACCGAAGATGTGAGGAGCGCGCTGGAGCCCTGCTGGA	651
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuLeuAlaThr	200
Db	652	CCGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAAGATTGGAGCTAGCCACT	711
Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluLeuAspLeuTrpGlyGluTrp	220
Db	712	GGCTACAAAGTGTATGGCGCTGCGGATGGAGAAAGAGAGGATTGTGGGGCAGTGG	771
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	772	AGCCCCATTTGTCTTCCAGACACCCCTTCTCTCCAAAGATGTGGGGTATCAGGG	831
Qy	241	AsnLeuCysGlyThrProGlyGlyGluProLeuLeuLeuTrpLysAlaProGlyPro	260
Db	832	AACCTCTGTGGAGCCTTGAGGAGAGAAACCTTTGCTTATGGAAGGCCCCAGGGCCC	891
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
Db	892	TGTGTGAGGTGAGCTACAAAGTCTGTTCTGGGTGAGGTGCTGAGCTGAGTCCAGAA	951
Qy	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
Db	952	GGAAATACCTGCTGCTCTCTTAAATTTCCAGTGGGGCGAGTGGGCGAGGTGTCGGCT	1011
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
Db	1012	GTCAAACCCCAACAGCTGGAGCCCTCTCACCAACCTCTCTTTGGTCTGCTTGGATTACGC	1071
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340

Db	1072	TCGTCCCCCGTGTAGCTGGGAGTCTCAGCAGCATCCTCGGAGCACGGAGTCTACTGGTGA	1131
Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
Db	1132	TGGCAACCGGGGCTGGGAAACCACTGAGCATGTAGTGGAGTGGGCTCGAGATGGGAC	1191
Qy	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
Db	1192	CCCTTGAGAAATCAACTGGGTCCGGCTTCCCTCGGAACTCAGTGTCTCTGTACCA	1251
Qy	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
Db	1252	GGGAATTTACTGTGGGGTCCCTATCGAATCACTGTGCCGCGAGTCTCTGTCTCAGGC	1311
Qy	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
Db	1312	TTGGCTCTGCATCTCCGTCTGGGGTTTCCAGGAGGAATTAGCACCCCTTAGTGGGGCCA	1371
Qy	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
Db	1372	ACGTTTGGCGACTCCAAAGATGCCCTCCAGGAGCCCGCCCATAGCTGGGAGAGGTC	1431
Qy	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
Db	1432	CCAAGGCACCAAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGA	1491
Qy	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
Db	1492	AGCCCTCCCTGTGCATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT	1551
Qy	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
Db	1552	CCTTGGGCTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGTGACAGGGCCCTCT	1611
Qy	501	GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly	520
Db	1612	GGTCCCATCTCCGGCTTCACTTACCAGATAACACCCCTGAGGTGGAAGTTCTGCCGGC	1671
Qy	521	IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
Db	1672	ATCCTATTCTTGTGGGCTTGTTCCTGTGGGTGTGGCTGAGCCCTGGCCACCTCTGGA	1731
Qy	541	ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp	560
Db	1732	AGTGCTACACCTTAAGGCACAAAGTGTCTCCCGCTGGGTCTGGGAGAAAGTTCTTGAT	1791
Qy	561	ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu	580
Db	1792	CCTGTCAACAGCAGTTCAGGCCAGCCCACTGAGCAAGTACCTGAGGCCAGCCCTT	1851
Qy	581	GlyAspLeuProIleLeuGluValGluMetGluProProValMetGluSerSer	600
Db	1852	GGGGATTTGCCCATCTCTGAAGTGGAGGAGATGAGCCCCCGCGGTATGGAGTCTCTCC	1911
Qy	601	GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr	620
Db	1912	CAGCCCGCCAGGCCACCGCCGCTTGTACTCTGGGTATGAGAGGACATCTCTCTGCCACA	1971
Qy	621	ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla	636
Db	1972	CCTGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC	2019

RESULT 8

US-10-000-776-11
; Sequence 11, Application US/10000776
; Publication No. US20020164609A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pflanz, Stefan K.-H.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, Jose F.
; APPLICANT: Rennick, Donna
; APPLICANT: de Waal Malefyt, Rene

; APPLICANT: Cheung, Jeanne
 ; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
 ; FILE REFERENCE: DX01040K3
 ; CURRENT APPLICATION NUMBER: US/10/000,776
 ; CURRENT FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 09/791,497
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: 09/627,897
 ; PRIOR FILING DATE: 2000-07-27
 ; PRIOR APPLICATION NUMBER: 60/146,581
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 60/147,763
 ; PRIOR FILING DATE: 1999-08-06
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 2628
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (112)..(2019)
 ; OTHER INFORMATION:
 ; NAME/KEY: misc.feature
 ; LOCATION: (2433)..(2433)
 ; OTHER INFORMATION: Unidentified base.
 ; US-10-000-776-11

Alignment Scores:
 Pred. No.: 1,92e-309 Length: 2628
 Score: 3494.00 Matches: 635
 Percent Similarity: 99.84% Conservative: 0
 Best Local Similarity: 99.84% Mismatches: 1
 Query Match: 99.89% Indels: 0
 DB: 13 Gaps: 0

US-10-088-950A-1 (1-636) x US-10-000-776-11 (1-2628)

QY	1	MetArgGlyValArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
DB	112	ATGCGGGAGGAGGAGGCGGCGCCCTTCTGGCTGTGGCGCGCTGCCAAGCTGGCGCTGCTG	171
QY	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
DB	172	CCTCTGTTGGTGGTGTCTTTCAGCGGACGGCTCCCGAGGAGCGCGCGGCGGCGGCTG	231
QY	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
DB	232	TGCTACGGAGTTGGACCCCTTGGCGGACTTGAACCTGCTCGTGGGAGGCTCTTGGGACCTG	291
QY	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
DB	292	GGAGCCCCCTCCGAGTTACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	351
QY	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
DB	352	GTGGCAGTGGCAGCGGAGCTGGTGGCCATCTCTCGGGAACAGCTCACCATGTCT	411
QY	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
DB	412	GACAAACTCTCTGTCTGGGGGCACTAAGGCGAGGCGGAGGCTCTCTGGGCGGCGGCT	471
QY	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValaPheSer	140
DB	472	AACCTAGAAACCCAAATGAAGCCAAACGCCCGCGGCTGGGCGGCTGACGTGACATTTCC	531
QY	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
DB	532	GAGGATGACCCCTCGAGGCGGAGCTGTCCATTTGGGCGGCGGCTGACATGCGGCTCAT	591
QY	161	ValLeuLeuLeuGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
DB	592	GTTCTGATCTGCCAGTTCCACTACCGAAGATGTGAGGAGGCGGCGGCTGAGCCCTGCTG	651

QY	181	ProGluLeuLysThrIleProLeuTrpProValGluIleGlnAspLeuGluLeuAlaThr	200
DB	652	CCGGAGCTGAAGACCATACCTCCCTGACCCCTGTTGAGATCCAGATTTGGAGTACCCACT	711
QY	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
DB	712	GGCTACAAAGTGTATGGCGCTGCCGATGAGAGGAGGAGGAGGATTTGTGGCGGCGAGTGG	771
QY	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
DB	772	AGCCCCATTTGTCTCCAGACACCCGCTTCTGCTCCAAAGATGTGTGGGTATCAGGG	831
QY	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
DB	832	AACCTCTGTGGGAGCGCTGGAGGAGGAGAACTTTGCTTCTATGGAAGGCCCGGCGGCC	891
QY	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
DB	892	TGTGTGAGGTGAGCTACAAAGTCTGTTCTGGGTGGAGTCTGTGAGTGTGAGTCCAGAA	951
QY	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
DB	952	GGATTTACCTGCTGCTCTCCCTAATCCAGTGGGCGGAGTGGGCGGAGTGTCCGCT	1011
QY	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
DB	1012	GTCAACGCCCAACAGCTGGGAGGCTCTCACCAACCTCTCTTGGTCTGTGGATTGAGCC	1071
QY	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
DB	1072	TCTGCCCCCGCTAGCGTGGCAGTCAAGCAGTCTGCTGGGAGCAGCGAGCTACTGTGACC	1131
QY	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
DB	1132	TGGCAACCGGGGCGCTGGGGAAACCACTGGAGCATGTAGTGGGCTGGAGATGGGGAC	1191
QY	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
DB	1192	CCCCCTGGGAAACCTCAACTGGGTGGGCTTCCCCCTGGGAACTCAGTGTCTGTACCA	1251
QY	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
DB	1252	GGGAATTTCACTGTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTTCAGGC	1311
QY	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
DB	1312	TTGGGCTCTGCAATCTCCGCTCTGGGGGTTCAGGGAGGAATTAGCACCCCTAGTGGGGCA	1371
QY	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
DB	1372	AGCTTTGGGAGCTCCAGATGCCCTCCAGGGACCCCGCCCATAGCTGGGGAGAGGTC	1431
QY	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
DB	1432	CCAAAGCCACGAGCTTCGAGGCGGCGGCTCCACCCACTACACCTGTGTGTGACAGAGTGA	1491
QY	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
DB	1492	AGCCCCCTCGTGTGATGAATGTGAGTGGGCAACACAGAGAGTGTACCTGTGCTGACCTT	1551
QY	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
DB	1552	CCTTGGGGTCTCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGAGGCGGCTCTCT	1611
QY	501	GlyProIleLeuArgLeuHisLeuProAspLeuThrLeuArgTrpLysValLeuProGly	520
DB	1612	GGTCCCATCTCCGCTTCTCATCTACAGATAACCCCTGAGGTGGAAGTCTGTGGCGGCG	1671
QY	521	IleLeuPheLeuTrpGlyPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
DB	1672	ATCCTATTCTTGTGGGGCTTGTCTGTGGGGGTGTGGGCTGAGCCTGAGCCACCTCTGGA	1731

Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1732 AGGTGCTACCACTAAGGCACAAAGTGTGCTGCCCGCTGGGTCTGGGAGAAAGTTCTCGAT 1791
Qy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1792 CCTGCCAACAGAGTTTTCAGGCCAGCCACATGAGCAAGTACCTGAGAGCCACGCCCTT 1851
Qy 581 GlyAspLeuProLeuLeuGluValGluGluMetGluProProValMetGluSerSer 600
Db 1852 GGGGACTTGCCCATCTGGAAGTGGAGAGATGAGAGCCCGCCGGTTATGGAGTCTCTCC 1911
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1912 CAGCCCGCCAGGCGCCCGCCCTTGACTCTGGGTATGAGAAGCACTTCTCTGCCACA 1971
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1972 CCTGAGGAGCTGGGCCCTTCTGGGGCCCCCAGGCGCCAGAGTTCTGGCC 2019

RESULT 9

US-10-777-790-11
; Sequence 11, Application US/10777790
; Publication No. US20040198955A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pfanz, Stefan K.-H.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, Jose F.
; APPLICANT: Rennick, Donna
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX01040K3
; CURRENT APPLICATION NUMBER: US/10/777,790
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/10/000,776
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112)..(2019)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2433)..(2433)
; OTHER INFORMATION: Unidentified base.
US-10-777-790-11

Alignment Scores:
Pred. No.: 1.92e-309 Length: 2628
Score: 3494.00 Matches: 635
Percent Similarity: 99.84% Conservative: 0
Best Local Similarity: 99.84% Mismatches: 1
Query Match: 99.89% Indels: 0
DB: 18 Gaps: 0

US-10-088-950A-1 (1-636) x US-10-777-790-11 (1-2628)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpProLeuProLysLeuAlaLeuLeu 20

Db 112 ATCGGGGAGCGAGGGCGGCCCTTTCTGGCTGTGGCCGCTGCCAAGCTGGCGCTCTG 171
Qy 21 ProLeuLeuTrpValLeuPheGlnArgTrpArgProGlnGlnGlySerAlaGlyProLeuGln 40
Db 172 CCTCTGTGTGGGTGCTTTTCCAGCGAGCGCTGCCAGGGCAGCGCGGGCCACTCGAG 231
Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 232 TGCTACGAGTTGGACCCCTTGGGCGACTTCAACTGCTCGTGGAGCCCTCTTGGGACCTG 291
Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
Db 292 GGAGCCCCCTCCGAGTTTACACCTCCAGAGCAAAAGTACCGTTTCCAAACAAACCCAGACT 351
Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaLeuProArgGluGlnLeuThrMetSer 100
Db 352 GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCGGGAACAGCTACCATGTCT 411
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120
Db 412 GACAAATCTCTGTGGGSCACTAAGGCAGGCCAGCCTCTCTGGCCCCCGTCTTCTGTG 471
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db 472 AACCTAGAAACCCCAATGAAGCCAAACGCCCGCGCTGGGCCCTGACGTGGACTTTTCC 531
Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
Db 532 GAGGATGACCCCTGGAGGCCACTGTCATTTGGGCCCCACCTACATGCCCATCTCTATAA 591
Qy 161 ValLeuLeuCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
Db 592 GTTCTGATCTGCCAGTTCCACTACCGAAGATGTCCAGAGCGCGCTGGACCTCTCGAA 651
Qy 181 ProGluLeuLysThrLeuProLeuThrProValGluLeuGlnAspLeuGluLeuAlaThr 200
Db 652 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAGATTTGGAGCTAGCCACT 711
Qy 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluLeuAspLeuTrpGlyGluTrp 220
Db 712 GGCTACAAAGTGTATGGCGCTCCCGGATGAGAAAGAGAGATTTGTGGGGAGTGG 771
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
Db 772 AGCCCCATTTGTCTTCCAGACACCGCCCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 831
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
Db 832 AACCTCTGTGGGACCGCTGGAGGAGGAACCTTTGCTTCTATGGAAGGCCCCAGGGGCC 891
Qy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280
Db 892 TGTGTGAGGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTCTGTGAGCTGAGTCCAGAA 951
Qy 281 GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
Db 952 GGAAATTACCTGTCTGTCTCCCTAAATTCAGTGGGGCGGAGTGGGCCAGGGTGTCCGCT 1011
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
Db 1012 GTCAACGCCACAAAGCTGGGAGCCTCTCACCACCTCTCTTTGCTGCTTGGATTACGCC 1071
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
Db 1072 TCTGCCCCCGGTAGCTGGCAGTCCAGCATCGCTGGGAGCAGGAGCTACTTGGTGACC 1131
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
Db 1132 TGSCAACCGGGGCTGGGGAACCATCTGGAGCATGTAGTGGACTGGGCTCGAGATGGGGAC 1191
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380

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Db 1192 CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCTTGGGAACCTCAGTCTCTGTACCA 1251
Qy 381 GlyAsnPhenValGlyValProTyrArgIleThrValThraValSerAlaSerGly 400
Db 1252 GGGAAATTCACCTGTCCGGGTCCCTATCAATCACTGTGACCGCAGTCTCTGTTCAGCG 1311
Qy 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1312 TTGGCCCTTCGCATCCCTCCGCTCTGGGGTTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA 1371
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db 1372 AGCTTTGGCGACTCAAGATGCCCTCCAGGGACCCCGCCATAGCGTGGGGAGAGGTC 1431
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db 1432 CCAAGGCACAGCTTCAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGGAAAC 1491
Qy 461 SerProSerValCysMetAenValSerGlyAenThrGlnSerValThrLeuProAspLeu 480
Db 1492 AGCCCTCCGCTGCAATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCTGACCTT 1551
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1552 CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT 1611
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAenThrLeuArgTrpLysValLeuProGly 520
Db 1612 GGTCCCATCTCCGGCTTCATCTACACAGATAACACCCCTGAGGTGGAAAGTTCTCGCGGC 1671
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1672 ATCCTATTCTTGGGGCTTGTTCCTTGTGGGGTGTGGCTGAGCTGGCCACCTCTGA 1731
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1732 AGTGTCTACCACTAAGGCACAAAGTGTGCCCGCTGGGTCTGGGAGAAAGTTCTCGAT 1791
Qy 561 ProAlaAenSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1792 CCTGCCAACAGCAGTTCAGGCCAGCCCCACATGAGCAAGTACCTGAGGCCAGCCCTT 1851
Qy 581 GlyAspLeuProIleLeuGluValGluMetGluProProValMetGluSerSer 600
Db 1852 GGGGACTTGGCCATCTCGNAGTGGAGAGTGGAGCCCCCGCGGTATGGAGTCTTCC 1911
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1912 CAGCCCGCCAGGCCACCGCCCGCTGACTCTGGGTATGAGAAGCACTTCTCTGCCACA 1971
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1972 CCTGAGAGAGTGGGCTTCTGGGGCCCCCCCCAGGCCACAGGTTCTGGCC 2019
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RESULT 10

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US-10-663-158-4
; Sequence 4, Application US/10663158
; Publication No. US2004023452A1
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederic
; APPLICANT: Grewal, Iqbal
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: TYPE I CYTOKINE RECEPTOR TCCR
; FILE REFERENCE: 11669.123USC1
; CURRENT APPLICATION NUMBER: US/10/663,158
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,542
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
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; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-663-158-4
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Alignment Scores:

Pred. No.:	5,95e-177	Length:	2005
Score:	2044.00	Matches:	388
Percent Similarity:	72.55%	Conservative:	61
Best Local Similarity:	62.78%	Mismatches:	161
Query Match:	58.43%	Indels:	8
DB:	18	Gaps:	3

US-10-088-950A-1 (1-636) x US-10-663-158-4 (1-2005)

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Qy 14 LeuProLysLeuAlaLeuLeuProLeuLeuTrpValLeuPheGlnArgThrArgProGln 33
Db 45 CTCAGCGCGTTGGAGCTTCTGCTGCTGTAATGCTGCTGCGGACGCGGGCCCCAC 104
Qy 34 GlySerAlaGlyProLeuGlnCysTyrGlyValGlyProLeuGlyAspLeuAsnCysSer 53
Db 105 GCGAGTCCAGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 164
Qy 54 TrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyr 73
Db 165 TGGGAACCTTTGGGCGACCTGGAGACTCCACTGTGCTGTATCACCAGAGTCAGAAATAC 224
Qy 74 ArgSerAenLysThrGlnThrValAlaValAlaAlaGlyArgSerTrpValAlaIlePro 93
Db 225 CATCCCAATAGACTCTGGGAGTGAAGGTGCTTCCAAACAAAGTTGGGTGACCAATCCC 284
Qy 94 ArgGluGlnLeuThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnPro 113
Db 285 CCGGACAGATTCCACCATGGCTGACAACTCTCATCTGGGGGACACAAAAGGCGGCT 344
Qy 114 LeuTrpProProValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeu 133
Db 345 CTGTGCTCTCTGCTCTGTGAACCTGGAGACCCCAATGAAGCCACAGACACCTCAGATC 404
Qy 134 GlyProAspValAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaPro 153
Db 405 TTCTCTCAAGTGGATATTCTGAGGAAGCAACCTTGGAGGCCACTGTGAGTGGGGCGCG 464
Qy 154 ProThrTrpProSerHisLysValLeuIleCysGlnPheHisTyrArgArgCysGlnGlu 173
Db 465 CCGGTGTGGCCACCCGACAGAAAGCTCTCACTGTGCTGCTGCTGCTGCTGCTGCTGCT 524
Qy 174 AlaAlaTrpThrLeuLeuGluProGluLeuLysThrIleProLeuThrProValGluIle 193
Db 525 GAAGCATGGACCCGCTGGAGCCCGCAGCTGAAGCAGATGGGCTGACTCTCTGTTGAGATG 584
Qy 194 GlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213
Db 585 GAGAACCTGGAAACCTGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
Qy 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaPro 233
Db 645 TATCCA--TGGGGCGAGTGGAGTTGCGCCCTGTCTCTCCAGACGCCATCTTAGATCT 701
Qy 234 LysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeu 253
Db 702 GAAGATGTGGGTATCGGGGACCGCTGTGTGAACCTCTTGGCAAAACGGGACGCCCTGCT 761
Qy 254 LeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTrpValGly 273
Db 762 GTCTGAGAGCCCAAGACCTTGTGTGAGGTGACTTACACAGTCTGGTTTGGGGCTGA 821
Qy 274 GlyArgGluLeuSerProGluGlyIleThrCysCysCysSerLeuIleProSerGlyAla 293
Db 822 GATATTACTACAACTCAAGAGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Qy 294 GluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAsnLeuSer 313
```

RESULT 11

APPLICANT: BODARY, SARAH C.

; APPLICANT:	CLARK, HILLARY
; APPLICANT:	BRISDELL, HUNTE
; APPLICANT:	JACKMAN, JANET
; APPLICANT:	SCHOENFELD, JILL R.
; APPLICANT:	WILLIAMS, P. MICKEY
; APPLICANT:	WOOD, WILLIAM I.
; APPLICANT:	WU, THOMAS D.
; TITLE OF INVENTION:	Compositions and Methods for the Treatment of Immune
; FILE REFERENCE:	P1948R1-US
; CURRENT APPLICATION NUMBER:	US/10/370, 715B
; CURRENT FILING DATE:	2003-02-21
; NUMBER OF SEQ ID NOS:	742
; SEQ ID NO 67	
; LENGTH:	4040
; TYPE:	DNA
; ORGANISM:	Homo sapien
US-10-370-715B-67	
Alignment Scores:	
Pred. No.:	1.58e-24
Score:	381.50
Percent Similarity:	28.18%
Best Local Similarity:	35.68%
Query Match:	10.91%
DB:	18 Gaps: 35
US-10-088-950A-1 (1-636) x US-10-370-715B-67 (1-4040)	
QY 12	TripProLeuProLysLeuAla-Leu-----LeuProLeuLeuTrpValLeuPhe----- 27
Db 883	TGCCCACTCCCTCAATTCTCAAGTCACAGCTTCCCCTGGTGACAACCTTGTTGTCTG 942
QY 27	----- 27
Db 943	CRAAACTGGCGTGATCAATAGTAGTAATCAAATTTCAAATATGTGGAGCAGAGATCTTCGTTGG 1002
QY 28	----GlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCysTyrcGly'valGlyPr 46
Db 1003	TGTTGCTCCAGAACACGCCTCAAAAT-----TTATCTGTCATACAGAAGGGAGA 1050
QY 46	oLeuGlyAspLeuAsnCyseSerTripGluProLeuGlyAsp----- 59
Db 1051	ACAGGGGACTGTGGCCCTGCACCTGGGAAGAGACGAGACACCACCTATACACTGAGTA 1110
QY 60	-----LeuGlyAlaProSerGluLeuHisLeuGlnSerGln----- 71
Db 1111	TACTCTACAGCTAAAGTGGACCCAAAAAATTTAACTGGCAGAGCAATGTAAAGACATTTA 1170
QY 72	-----LysTyArgSerAsnLysTh----- 78
Db 1171	TTGTGACTATTGGACTTTGGAAATCAACCTCACCCCTGAATCACTGAAATCCAATTTCCAC 1230
QY 78	rGlnThrVal---AlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLe 97
Db 1231	AGCCAAGGTTACTGCTGCTCAATAGCTTGGAGCTCCTCTTCATTTCCA---TCCACATT 1287
QY 97	uThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr 117
Db 1288	CACATTTCTTGGACATAGT-----AGGCCTCTT---CCTCC 1320
QY 117	oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProaspVa 137
Db 1321	GTTGGGACATTAGAAATCAAATTTCAA---AAGGCTTCCGTGAGCAGA----- 1363
QY 137	lAspPheSerGluAspAppProLeuGluAlaThrValHisTrpAlaProProthrTrpPr 157
Db 1364	-----TGTACCCCTTTATTGGAGA-----GA 1383
QY 157	oSerHisLysValLeuIleCysGlnPheHisTyArgArgCysGlnGluAlaAlaTrpTh 177
Db 1384	TGAGGGACTGTGACTGCTTAATCGACTACAGATATCGGCCAGCATTAACAGCAGGCTCTGGAA 1443

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177 rLeuLeuGluProGluLeuLysThrIleProLeuThrProVal-----GluIle 193
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1444 TATG-----GTTAATGTTACAAAGGCCAAAGGAGACATGATTT 1482
    : : : : :
193 eGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysG1 213
    : : : : :
1483 GCTGGATCTGAACACCATTTACAGAAATATGAAATTCCTCCTAAGCTACATCTTTA 1542
    : : : : :
213 uGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPro-----Pr 230
    : : : : :
1543 TAAGGAAGTTGGAGTGTGAGTGAATCATTTGAGAGCACAACACAGAGAGAGGCC 1602
    : : : : :
230 oSerAlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluG1 250
    : : : : :
1603 TACTGGGATGTTAGATGTCGTGTACATGAACCGCACATTTGACTAC---AGTAGACAACA 1659
    : : : : :
250 uProLeuLeuLeuTrpLys-----AlaProGlyProCysValGlnVa 264
    : : : : :
1660 GATTTCTCTTTCTGGAAGAACTGAGTGTCTCAGAGGCGAGAGAAATTCCTCCACTA 1719
    : : : : :
264 lSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu-----GlyIle 282
    : : : : :
1720 TCAGGTGACCTTCAGAGCTGACAGAGGAGAAAGCCATGACACAGAACATCACAGAGACA 1779
    : : : : :
282 eThrCysCysSerLeuLeuLeuProSerGlyAlaGluTrpAla---ArgValSerAlaVa 301
    : : : : :
1780 CACCTCTCTGACACACATCTTCTAGAACCGGAATCGGCTGTGTGTCTGCGACG 1839
    : : : : :
301 lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe 319
    : : : : :
1840 AAATTTAAAGGAGCTTCTCGCCACTCGTATTACATAATCAACCTGTGTGAGCAGG 1899
    : : : : :
319 rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa 339
    : : : : :
1900 GTTGCTGCTCTCTCGCAGCTCTCTGCAACTCA---GAGGCGATGAGCAACATCTGTGT 1956
    : : : : :
339 lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl 356
    : : : : :
1957 GACTTGGCAGCTCTCCAGGAAAGATCTCTGCTGTTCCAGGATGAGTGTGTGGAATGGAG 2016
    : : : : :
356 aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProG1 373
    : : : : :
2017 AGACCTCATCCAGGGGTGACACACAGGTCCTCTAAACTGGCTACGGAGTGCACCTTA 2076
    : : : : :
373 yAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVa 393
    : : : : :
2077 CAATGTGTCTGCTCTGATTTTACAGAAACATAAAATCCTATCTGTTATGAATTCGTGT 2136
    : : : : :
393 lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluG1 413
    : : : : :
2137 GTATGCACTCTCAGGGAT---CAAGGAGGATGTCAGCTCCATCTGGGTAACTTAAGCA 2193
    : : : : :
413 uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr 433
    : : : : :
2194 CAAGACACCACTGAGTGGCCCCCAATTAATGTCATCACAGAG---GANAAGGGAGCAT 2250
    : : : : :
433 oAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrTh 453
    : : : : :
2251 TTTAATTTTCATGGAACAGCATCTCCAGCCAGAGCAAAATGGGCTGCTCTCCATATAG 2310
    : : : : :
453 rLeuCys-----AlaGlnSerGlyThrSerProSerValCys-----MetAs 467
    : : : : :
2311 GATATCTGGAAGAACGGAGCTCCAACTCCAGCTCAGCTCTGTGAAATTCCTACAG 2370
    : : : : :
467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
    : : : : :
2371 AGTCTCCCAAAATTCACATCCCAATAAACAGCCTGAG---CCCCAGTGACATATGCTCT 2427
    : : : : :
487 utrpValThrAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHi 507
    : : : : :
2428 GTGGATGACAGCTCTGACAGCTGCTGTGGTGAAGTTCCCAAGGAAATGAGAGGAATTTG 2487
    : : : : :
507 sLeuProAspAsnThr-LeuArgTrpTrpLysValLeuPro-----GlyIleLeuPheL 524
    : : : : :
2488 TCTGCAAGGTAAAGCCAAATTTGGATGGCGTTTGTGGCACCAGCAATTTGCATTGCTATCAT 2547
    : : : : :
524 euTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrH 544
    : : : : :
2548 CATGGTGGGCAATTT-----TCTCAACGCAATTAATCTCCAGCAAAAAGGTGTTGT 2595
    : : : : :
544 iLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnS 564
    : : : : :
2596 T-CTCTAGCAGCCCTCAGACCTCAGTGTGTAGCAGAGAAATTCAGATCCAGCAATA 2654
    : : : : :
564 erSerSerGlyGlnProHis-----MetGluGlnValProGluAlaGlnP 579
    : : : : :
2655 GCATTTGGCTAAGAAATATATCCATTCAGAGAGAGAGACACAGCTGCCCTTGGACAGCG 2714
    : : : : :
579 roLeuGlyAspLeuProIleLeuGluValGluMetGluProProPro-----595
    : : : : :
2715 TCCTGATAGACTGGCCCGCCGCTGAA-----GATCTGAAACGCTGGTGCATCA 2762
    : : : : :
596 -----ValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu-----609
    : : : : :
2763 GTGAGTCTCTTCA-TCAAGTGACCCCGAGTTTTCAGACATCCCCCTGCTCCAACCTGGCCA 2821
    : : : : :
610 -----AspSerGlyTyr-GluLysHisPheLeuProThrPro 621
    : : : : :
2822 CAAGGGGAAAAGGAATFCCAAGGTTCATCAGGCTCTGAGAGAAAGACATGATGCACAGTGCC 2881
    : : : : :
622 GluGluLeuGlyLeuLeuGlyProProArgProGlnValLeu 635
    : : : : :
2882 TCA-----AGCCACACCTCCAGAGACTCTC 2908
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RESULT 12
US-10-398-666-11
; Sequence 11, Application US/10398666
; Publication No: US20040073021A1
; GENERAL INFORMATION:
; APPLICANT: BIOTECHNOLOGY RESEARCH AND DEVELOPMENT CORPORATION
; TITLE OF INVENTION: CLONING AND SEQUENCING OF THE PORCINE INTERLEUKIN-12
; TITLE OF INVENTION: RECEPTOR BETA-1 AND BETA-2 CHAINS
; FILE REFERENCE: 21419/92796
; CURRENT APPLICATION NUMBER: US/10/398,666
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4023
; TYPE: DNA
; ORGANISM: Porcine sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (230)..(2812)
US-10-398-666-11

Alignment Scores:
Pred. No.: 6,55e-20 Length: 4023
Score: 331.00 Matches: 174
Percent Similarity: 37.63% Conservative: 86
Best Local Similarity: 25.18% Mismatches: 263
Query Match: 9.46% Indels: 170
DB: 17 Gaps: 35

US-10-088-950A-1 (1-636) x US-10-398-666-11 (1-4023)
QY 31 ArgProGlnGlySerAlaGlyProLeuGlnCysTyrGlyValGlyProLeuGlyAspLeu 50
    : : : : :
Db 605 CAGCCTCAAAAC-----GTATCTTGTATGCAAGGAGAGACGTGGGACAGTG 652
    : : : : :
QY 51 AsnCysSerTrpGluProLeuGlyAsp-----LeuGlyAlaProSerGluLeuHisLeu 68
    : : : : :
Db 653 GCCTGAGCTGGGACAGAGACGATGCCATCTATATCTATCTATCTTACAAATTA 712
    : : : : :
QY 69 -GlnSerGlnLysTyrArgSerAsnLysThrGlnThrValAlaValAlaAlaGlyArgSe 88
    : : : : :

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Db 713 AATGACCAAAA-----ATTAACTTGGCAGAG 742
 Qy 88 rTrpValAlaIleProArgGluGlnLeuThrMetSerAspLysLeuVal-----Tr 106
 Db 743 CAATGTAGCGATT-----ATTATGTGACTTTG 772
 Qy 106 pGlyThrLysAlaGlyGlnProLeuTrpProValPheValAsnLeuGluThrGlnMe 126
 Db 773 GACCTTGAATCAACCTACCGCTG-----AATCACCTGAATCTAGTTACACAG-- 821
 Qy 126 tLysProAsnAlaProArgLeuGlyProAspVal----- 137
 Db 822 -----CCAGGTTACTGCCCATCAATAGTCTAGGACTGCGCTTCAATTC 868
 Qy 138 -----AspSerGluAspAs 143
 Db 869 TGCACATTTCACATTTGGATGTAGTAGGCTCTTCTCGTGGGACATCAGAAATCAA 928
 Qy 143 pProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHis---LysValle 162
 Db 929 TGT-GTAAATGCCCTCCGTGAGCACATGTACCCTGCAATGGAGAGATGAGGGCTAGTGCT 987
 Qy 162 uileCysGlnPheHisTrpArgArgCysGlnGluAlaTrpThrLeuLeuGluProG 182
 Db 988 GCTTAATCGACTAGATACCGGCTGTTTACAGCAGATCCTGGAAATATGGTTAAT- 1042
 Qy 182 uLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThrGlyTy 202
 Db 1043 ----GCTACAAATGCCAAAGGAGACATGATTTGGTGAATCTGAAACCTTTACAGAA 1098
 Qy 202 rLysValTyArgCysArgMetGluLysGluAspLeuTrpGlyLeuTrpSerPr 222
 Db 1099 TGAATTTTCAGATTTCTTAAGCCACATCTTCAAGAGGAGTAGATGAGTATGGAGTGA 1158
 Qy 222 oileLeuSerPheGlnThrPro-----ProSerAlaProLysAspValTrpValse 239
 Db 1159 ATCAATGAGAACTCAAACTCCAGAGAAAGAGCTTACAGGAGTGTAGACCTGCTGTAT 1218
 Qy 239 rGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLys----- 256
 Db 1219 GAAACAGCACATTGACTACAAA---AGACAACAGATTATCTTTCTGGAGAAATCTGAG 1275
 Qy 257 -----AlaProGlyProCysValGlnValSerTyLysVal----- 268
 Db 1276 TCTATCAGAGCAAGAGGAAAAATCCTCCAC-----TATCAAGTGAACCTTGCAGGAGGT 1329
 Qy 269 -----TrpPheTrpValG 273
 Db 1330 CGCAGAGGGGAATGCCACACTGCAGAAATATCACTGAACGCAACTCCTGGACCTGGACC-- 1387
 Qy 273 yGlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuIleProSerGlyAl 293
 Db 1388 -----ATACCAGAACTGG 1401
 Qy 293 aGluTrp---AlaArgValSerAlaValAsnAla-----ThrSerTrpGluProLeuTh 310
 Db 1402 CATCTGGGCTGGCGCGCTGTCTGAGCTAACTCCAAAGGAGTTCCTGCCCACTCGTAT 1461
 Qy 310 rAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSe 330
 Db 1462 TAAATAGACAGACTGTGCGGAGCAGCGGTTGCTGGCTCCTCAGCAGGTTTCTGCAAAACC 1521
 Qy 330 rIleAlaGlySerThrGluLeuLeuValThrTrp---GlnProGlyProGlyGluProLe 349
 Db 1522 A---GAGGCTGGACAACTCTCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1578
 Qy 349 u-----GluHisValValAspTrpAlaArg-----AspGlyAspProLeuGluLy 364
 Db 1579 TGTGAGGAGTATGTGTGGAGTGGAGGAGTCCATCTCAGGGGTGGCATGCGAGCCCC 1638
 Qy 364 sLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuProGlyAsnPheTh 384
 Db 1639 TCTAAGCTGGCTGGGAGTCCCCCTTACAAACACAGCTGCCCTCATCTCTCAGAACACATA 1698

Qy 384 rValGlyValProTyArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSerAl 404
 Db 1699 ACCCTACATCTGTTATGAATCCGAGTGCACGCACTTTTTCAGGGGAC---CAGGAGGATG 1755
 Qy 404 aSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyProThrLeuTrpAr 424
 Db 1756 CAGCTCCATCCGGGTGACTTGAAGCATAAAGCACCACCTAGTGGCCCCCACCATTAAATGC 1815
 Qy 424 gLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyLeuValProArgHisG 444
 Db 1816 CATCTCAGAG---GAAAGGGGAGCAATTTAATTTTCATGGGAGCAAAATTCAGCCCCAGGA 1872
 Qy 444 nLeuArgGlyHisLeuThrHisTyThrLeuCys-----AlaGlnSerGlyThrSe 461
 Db 1873 GCAAAATGGCTGCATCTCCATACAGATCTATTGAAGGACGGGACTCCGATTCCTCCA 1932
 Qy 461 rProSerValCys-----MetAsnValSerGlyAsnThrGlnSerValThrLeuPr 478
 Db 1933 GCCTCAGCTCTGTAATTCCTTATAGAGTCTCCCCAAATCACATCCCATCAATAGCCT 1992
 Qy 478 oAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnG 498
 Db 1993 GCAG---CCAGAGTGACATACGCTGCTGTGATGACAGCTCTGACAGCTGCTGGCGAAAG 2049
 Qy 498 yProProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLys----- 516
 Db 2050 CCCCCAAGGAATCAGAGGGAATTTTGTCTG---CAAGGTAAAGCCAAATTTGGACACATT 2106
 Qy 517 -ValLeuProGlyIle-----LeuPheLeuTrpGlyLeuPheLeuLeuGlyCysG 533
 Db 2107 TGTAGCACCAAGCATTTGCTATGCTGTATCAGATGAGCTGCTGCTGCTGCTGCTGCTGCT 2152
 Qy 533 yLeuSerLeuAlaThrSerGlyArgCysTyThrHisLeuArgHisLysValLeu----- 550
 Db 2153 -----TCAATGCTGCTTCCGCGCAAAAGGTATTTGTTCTCTCTTTTGGC 2196
 Qy 551 -----ProArgTrpValTrpGluLysValProAspProAlaAsnSerSerSerGlyG 568
 Db 2197 CCTCAGACCTCAGTGTGTAGCAGAGAAATTCAGACCCAGCCCAATAGACATTTGGGCCAA 2256
 Qy 568 nProHis-----MetGluGlnValProGluAlaGlnProLeuGlyAspLe 583
 Db 2257 GAAATATCCATTTGTGGAGGAGAAAGAACAGCTGCTCCTGGATAGGCTCTCTGGCAGATG 2316
 Qy 583 uProIleLeuGluValGluMetGluProProProValMetGluSerSerGlnProAl 603
 Db 2317 GCCCACTCTGAA-----GAACTGAGCCCTGCTCATCAATGA-AGTCCCTTC 2363
 Qy 603 aGlnAlaThrAlaProLeuAspSerGlyTyThrGluLysHisPheLeuProThrProGluG 623
 Db 2364 CTCAAGTACTCAGTCTTCAGAG-----CCCCCATCATCCTCCA 2402
 Qy 623 uLeuGlyLeuLeuGlyProProArgProGln 633
 Db 2403 ACTGGCCAGGAAAGGACAAAGGCTCCAAG 2433

RESULT 13

US-10-641-643-1086
 ; Sequence 1086, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; Suan G. Stuart
 ; Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA

Qy	50	LeuAsnCyS	SerTrrpGluProLeuGlyAspLeuGlyAlaProSerGlnLeuHisLeuGln	59
Dd	587	CtCATCGCAGCTGGGACGAGCACTTGAGACCACCACTCCACCACTTCACCTCTGAAG	646	
Qy	70	SerGlnLysTyrArgSerAsn---	LysThrGlnThrValAlaVal-----	83
Dd	647	AGTTTCAGAGCGCGGGCAACTGTCTAGACCACAAGGGAACTCCATCTTGAGACTCGCTGGCCC	706	
Qy	84	AlaAlaGlyArgSerTrrpValAlaIleProArgGluGlnLeuThrMetSerAspLysLeu	103	
Dd	707	AGGACGGGCAGAGCACTGCTGCATCCACGCAACACCTGCTGTGTGTACCAAGAATAG	766	
Qy	104	LeuValTrrp-----	GlyThrLysAlaGlyGlnProLeuTrrp----	115
Dd	767	GGCATCTGGGTGCAGCGCAGAGAATCGCGTGGGGACCAAGCATGCCCAACACATGTGTCTT	826	
Qy	116	-----	ProProValPheValAsnLeuGluThrGlnMet	126
Dd	827	GATCCCCATGGATGTTGTGAACCTGGAGGCCCCCATGCTGCGGACCATGGACCCCAAGCCCT	886	
Qy	127	LysProAsnAlaProArgLeuGly---	-----ProAspValaspPhe	139
Dd	887	GAAGCGGCCCTCCCGAGCAGGCTGCCTACAGCTGTGCTGGGAGCCA-	-----	934
Qy	140	SerGluaspAspProLeuGluAlaThrValHisTrrpAlaProProThrTrrpProSerHis	159	
Dd	935	-----	TGGCAGCCAGGCGCTGCACATAAATCAG	961
Qy	160	LysValLeuIleCysGlnPhe---HisTyrArgArgCysGlnGluAlaAlaTrrpThrLeu	178	

QY 490 rAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgIleuHisLeuProAs 510
 Db 2014 CCTGATGACCTTGGACCCAGAGGGGTGCG- - - - -GAGCTACACATC- - - - - 2053
 QY 510 pAsnThrLeuArgTrpLysValLeuProGlyLysLeuPheLeuTrpGlyLeuPheLeuLe 530
 Db 2054 - - - - -ATCCTGGGCGCTGTTCGGCCCTCCCTGCTGTT 2082
 QY 530 u- - - - -GlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTrpHisLeuArgHi 547
 Db 2083 GCTCACCTGCCTCTGTGA- - - - -ACTGCCTGGCTCTGTTGCAGCCCAACAG 2130
 QY 547 sLysValLeuProArgTrpValTrpGluLysValProAspProAlaHisSerSerG1 567
 Db 2131 GAAG- - - - -AATCCCTCTGGCCAAAGTGTCCAGACCCAGCTCACAGCAGCCTGGG 2181
 QY 567 y- - - - -GlnProHisMetGluInValPro- - - - -GluAlaG1 578
 Db 2182 CTCTGGGTGCCCAATATGAGGAGGATGCTTCCAGCTGCCCGGCTTGCACGCC 2241
 QY 578 nProLeuGlyAspLeuProIleLeuGluValGluMetGluProPro- - - - - 595
 Db 2242 ACCATCACCAGCTCACAGTGTGGAGGAGTGAAGAGCGGTGCTGGGAGTC 2301
 QY 596 - - - - -ValMetGluSe 599
 Db 2302 CCATAACAGCTCAGAGACCTGTGGCCTCCCACTCTGTGTCAGACCTATGTGTCACAGG 2361
 QY 599 rSerGlnProAlaGlnAlaThrPro- - - - -LeuAspSerGlyTrpGluLysHisPheLe 618
 Db 2362 GGACCCCAAGACGATTTCCACCCAGCCCAATCCAGCTCTGGCACCGCATCAGGTCCT 2421
 QY 618 u- - - - -ProThrProGluGluLeuGlyLeuGlyPro- - - - - 629
 Db 2422 TTATGGCAGCTGTGGGAGCCCAACAGCCAGGAGCCAGGCA-CTATCTCGCTGTG 2480
 QY 630 - - - - -ProArgProGlnValLeu 635
 Db 2481 ACTCCACTCAGCCCTCTTGGGGGCTCACCCTCCAGCCCAAGTCCTA 2529

RESULT 14

US-10-252-157-457
 ; Sequence 457, Application US/10252157
 ; Publication No. US20030190640A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fatis, Mary
 ; APPLICANT: Pearson, Cecelia I.
 ; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
 ; FILE REFERENCE: PA-0027-1 US
 ; CURRENT APPLICATION NUMBER: US/10/252,157
 ; CURRENT FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: 60/295,048
 ; PRIOR FILING DATE: 2001-05-31
 ; NUMBER OF SEQ ID NOS: 501
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 457
 ; LENGTH: 3139
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030190640A1 346686.23
 US-10-252-157-457

Alignment Scores:
 Pred. No.: 5.67e-17 Length: 3139
 Score: 297.50 Matches: 173
 Percent Similarity: 34.73% Conservative: 76
 Best Local Similarity: 24.13% Mismatches: 269
 Query Match: 8.50% Indels: 201
 Db: 16 Gaps: 33

US-10-088-950A-1 (1-636) x US-10-252-157-457 (1-3139)
 QY 50 LeuAsnCysSerTrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGln 69
 Db 726 CTGATCTGCCAGTGGGAGCCAGGACCTGAGACCCACCTACCCAGCTTCACCTCTGAAG 785
 QY 70 SerGlnLysTrpArgSerAsn- - - - -LysThrGlnThrValAlaVal- - - - - 83
 Db 786 AGTTTCAAGACCGGGGCAACTGTCAAGACCAAGGGGACTCCATCTGGACTGCGTGCC 845
 QY 84 AlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSerAspLysLeu 103
 Db 846 AAGACCGGAGAGCCACTCTGCTATCCACGAAACACCTGTGTTGTACCAAGATATG 905
 QY 104 LeuValTrp- - - - -GlyThrLysAlaGlyGlnProLeuTrp- - - - - 115
 Db 906 GGCATCTGGGTGAGGAGAGATGCGTGGGACCCAGCATGTCCTCCCACTGTGTCTT 965
 QY 116 - - - - -ProProValPheValAsnLeuGluThrGlnMet 126
 Db 966 GATCCCATGATGTTGTGAACCTGGAGCCCTCATGCTGGGACCATGGACCCAGCCCT 1025
 QY 127 LysProAsnAlaProArgLeuGly- - - - -ProAspValAspPhe 139
 Db 1026 GAAGCGGCCCTCCCGAGGAGGCTGCCTACAGCTGTGTGGGAGCCA- - - - - 1073
 QY 140 SerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHis 159
 Db 1074 - - - - -TGGCAGCCAGGCTGCACATAAATCAG 1100
 QY 160 LysValLeuLeuCysGlnPhe- - - - -HisTyrArgArgCysGlnGluAlaIleTrpThrLeu 178
 Db 1101 AAG- - - - -TGTGAGCTGCCACAGCCGCGTGGAGAGGACGACGTGGGCACTG 1151
 QY 179 LeuGluProGluLeuLysThrIleProLeuThrProValGluLeuGlnAspLeuGluLeu 198
 Db 1152 GTGGGCCCT- - - - -CTCCCTTGGAGGCCCTTCATGATGAGCTC 1190
 QY 199 - - - - -AlaThrGlyTrpLysValTyrGlyArgCysArgMetGluLysGlu 213
 Db 1191 TGGGGGCTCTCCAGCCAGCGCTACCCCTGAGATACCTGCTGATCCGCTGGGCCCTG 1250
 QY 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThr- - - - -ProProSerAlaPr 233
 Db 1251 CCTGGCCACTGGAGCAGCTGGAGCCCGCAGCTGGAGCTGAGAACTACCGAAGCGGCCCT 1310
 QY 233 oLysAspValTrpValSerGlyAsnLeuCysGly- - - - -ThrProGlyGlyGluGluPr 251
 Db 1311 ACTGTCAGACTGGACACATGTTGGCGGCGCAGAGGAGCTGGACCCAGGA- - - - -CAGTG 1364
 QY 251 oLeuLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTr 271
 Db 1365 -CAGCTGTTCTGGAAG- - - - -CCAGTGCCCTGGAGGAGAGCAGCGGAGGATCAAGGTTA 1420
 QY 271 pValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysCysSerLeuIleProSe 291
 Db 1421 TGTG- - - - -GTTCTCTGGAGCCCTC 1441
 QY 291 rGlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAs 311
 Db 1442 AGCGAGGCTGGGGCCATCTCTGCCCTCTGCAACACACACAGAGCTCAGCTGCACCTTCCA 1501
 QY 311 nLeu- - - - -SerLeuValCysLeuAspSerAla- - - - -SerAl 322
 Db 1502 CTGCGCTTCAGAACGCCAGAGGTGGCCCTTGTGGCTATACTACGCGGGACCTCTCG 1561
 QY 322 aProArgSerValAlaValSerSerIleAlaGlySerThr- - - - - 335
 Db 1562 CCCCACCCGGTGTCTTCTCAGAAAGCAGAGGCCCGCCAGCTCTGACCCAGACTCCATGCCAT 1621
 QY 336 - - - - -GluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuG1 350
 Db 1622 GGCCCGAGACCTCTCACAGGCTCTGGGTAGGTGGAGCGCCCAATCCATCCATGGCGCTCAGG 1681

[illegible]

Db 1842 CATGAAACAACTACACACATTTTGTGTCAGGTTAAATCCCAATATGAGAA----- 1892
Qy 176 TrpThrLeuLeuGluProGluLeuLeuLeuThrIleProLeuThrProValGluIleGlnAsp 195
Db 1893 ---GTGATTGATGAGCAACAATGTTCTGTCCACATGAGCGCAAACTACCTCTTCAGTGAT 1949
Qy 196 LeuGluLeuAlaThrGlyTyrLeuValTyrGlyArgCysArgMetGluLeuGluAsp 215
Db 1950 CTGGATCCAGACACAAAGTACAAGCTTTTGTGCTGTGTGCAAGTGCACCACTCTCTGG 2009
Qy 216 LeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaProLys--- 234
Db 2010 AATGGAGGACTGGACCCAA---AAAGAGTTACAGCACCCGAGACTGCTCCCTCACAG 2066
Qy 235 -----AspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeu 252
Db 2067 GCTCTTGATGTG-----AGACAAGTGTGTCGGGAGATGGAAGACCAATTGTGACT 2120
Qy 253 LeuLeuTrpLysAlaProGlyProCysValGln-----ValSer 265
Db 2121 TTATTTCTGGAAG-----CCACTATTAAATACAGGCCAATGCGCAAAATCATATCC 2171
Qy 266 TyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGluGlyIleThrCysCys 285
Db 2172 TATAATATA-----GTTGTAGAAAATGAAGCCAAACCACTAGTCAGAACACTAC 2222
Qy 286 CysSerLeuIleProSerGlyAlaGluTrpAla----- 296
Db 2223 TGT-----GTCTGGGCCACCGCTCAGCACAAACCTGAGCCTT 2261
Qy 297 -----ArgValSerAlaValAsnAlaThrSerTrpGluProLeu 309
Db 2262 GACCTGCAACCTTACAGATTCGATCAGCAACCAACAGCATGGGGCATCTCCT--- 2318
Qy 310 ThrAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSer 329
Db 2319 GAGTCCTTGATGTCCTTCTTAAATGTCCTTGGACAGGTCAAGGAAAGACAATTA 2378
Qy 330 SerIleAlaGlySerThrGluLeuValThrTrpGlnProGlyProGlyGluProLeu 349
Db 2379 GGTATAAAGGATGCATTCAAT-----ATTCTTGGAGCCCGTATCTGGAGACAGATG 2432
Qy 350 GluHisValValAspTrp---AlaArgAspGlyAspProLeuGluLysLeuAsnTrpVal 368
Db 2433 GGCTATGTTGTGACTGGTGTGCACATTCACAGCAACCGCTGTGATTTGCAGTGAAG 2492
Qy 369 ArgLeuProProGlyAsnLeuSerAlaLeuLeuProGly---AsnPheThrValGlyVal 387
Db 2493 AACCTTGGTCCCAATACCAAGACCCACCATCCTCAGATGATTTTAAACCCAGGCGTC 2552
Qy 388 ProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSer---AlaSerSer 406
Db 2553 CGTTACAACTTCAGATTTTGAAGTCTGTGGACACAAAGCTCGGTTAGTAGAGAAA 2612
Qy 407 ValTrpGlyPheArgGluGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGln 426
Db 2613 CAAAGAGGATACACCCAGGAATCGCTCTTGTGTAATCCAAAGTG----- 2660
Qy 427 AspAlaProProGlyThrPro-----AlaIleAlaTrpGlyGluValProArgHis 443
Db 2661 GAGATTCCTTACTCGACCCCTAACTCCTCGTTGATGTGTAATCCAAAGGATGCGAGTGC 2720
Qy 444 GlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSer----- 458
Db 2721 TTCAGGCTGTTTATAAAGGGTACCTCGTGTATGTGTAATCCAAAGGATGCGAGTGC 2780
Qy 459 -----GlyThrSerProSerValCysMetAsnVal 468
Db 2781 AACCAACCTCGGAAAGGACCTCTTCCAGATAATTCAGTCTCTGTAAATACGACATC 2840
Qy 469 SerGlyAsn---ThrGlnSerValThrLeuProAspLeu---ProTrpGlyProCysGlu 486
Db 2841 AATGGCTCAGAGACAAAGACACTCACCGTGGAAAAACCTTCAGCCAGAGTCCCTCTATGAG 2900

Qy 487 LeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProGlyProIleLeuArgLeu 506
Db 2901 TTTTTCGTCACTCCGTACACCGCGCTGGCCAGGACCCCAATGAACGTTCCACAAAGGTC 2960
Qy 507 HisLeuProAspAsnThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpGly 526
Db 2961 ACAACTCCAGAT-----GCACGCTCCACATGCTGTCGAGATCATACTACCCATGACC 3014
Qy 527 LeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArg 546
Db 3015 CTCTGGCTCTTG-----CTCAGCATCATTTGTC-----TGCTACTGG----- 3050
Qy 547 HisLysValLeuProArgTrpValTrpGluLys-----ValProAspProAla 562
Db 3051 -----AAAAGTCAGTGGGTGAAGGAGAGTGTACCTGCACATTCCTCAATCCGTAC 3101
Qy 563 AsnSerSer----- 565
Db 3102 AAGAGCAGCATTTCTGTCACTCATATAAATCCAAGAAGATCCTCACTTAATAATGAATGTC 3161
Qy 565 ----- 565
Db 3162 AAAGACTGCATTCACAGATGCTTTGAAGTGATTAACAAGACGAGGACCAAGACACAG 3221
Qy 566 -----SerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeuGlyAsp 582
Db 3222 TGTGTAGGCTCTGGGAAACTTCACATTTGAAGATGTACCCACTAAGCGGCCAATC----- 3275
Qy 583 LeuProIleLeuGluValGluGluMetGluProProValMetGluSerSerGlnPro 602
Db 3276 GTGCCA---ACAGAAAAGGATTCCTCAGGCGCTGTGCTGCATCTCTTTTGAGAATTTT 3332
Qy 603 AlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeu----- 618
Db 3333 ACTTACGATCAGTCAGCTTTTGACTCTGGT-----TCCCATGGCCTCATTCAGGTGCC 3386
Qy 619 -----ProThrProGluGluLeuGlyLeuLeuGlyProPro 630
Db 3387 CTAAAGACACAGACACACACCACTTGACATTTGGCTCCACCT 3428

Search completed: February 23, 2005, 09:15:24

Job time : 997 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 04:25:18 ; Search time 5411 Seconds
(without alignments)
4474.011 Million cell updates/sec

Title: US-10-088-950A-1

Perfect score: 3498

Sequence: 1 MRGGRGAPFWLPLPKALL.....FLPTPEELGLLGPFPQVLA 636

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QMT=fastcap -SUFFIX=rstc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US10088950 @CGN 1 1 3437 @runat_18022005_094500_21835 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1734.5	49.6	2935	3 AK040457	Mus muscu
2	1376	39.3	900	4 BG756328	602713647
3	1281.5	36.6	783	7 CK000257	AGENCOURT
4	1251	35.8	942	5 BQ957232	AGENCOURT
5	1225	35.0	896	4 BF984779	602308006
6	1201.5	34.3	911	5 BQ919454	AGENCOURT
7	1170.5	33.5	681	2 BF035293	601457184
8	1125	32.2	620	7 CV030371	9471 Full
9	1104	31.6	950	5 BQ927024	AGENCOURT

10	1082.5	30.9	1028	5	BM917928	BM917928
11	1065	30.4	731	4	BI905856	AGENCOURT
12	1057	30.2	942	4	BG332437	603062945
13	1017	29.1	821	7	CO880024	602432807
14	990	28.3	803	7	CF785854	BovGen. 08
15	961	27.5	570	2	AW575269	AGENCOURT
16	911	26.0	427	7	CN790247	UI-HF-BKO
17	878	25.1	497	5	BN283853	4124813 B
18	864	24.7	579	5	BP337994	60233853
19	863.5	24.7	1776	4	BG115874	602316865
C 20	862	24.6	660	5	EX919538	602316865
C 21	862	24.6	660	5	EX919538	602316865
22	851	24.3	713	7	CK834168	4058370 B
23	839	24.0	597	4	BM048281	603627680
24	838	24.0	447	7	CN287418	170006000
25	832	23.8	674	6	CB422972	596137 MA
26	807	23.1	467	2	BF827655	MR2-HN003
27	804	23.0	653	7	CN789181	4133608 B
28	790.5	22.6	567	4	B1847463	469302 MA
29	784.5	22.4	772	4	B1559169	603241254
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31	781	22.3	710	4	BM761233	K-EST0041
32	781	22.3	711	4	BM760781	K-EST0041
C 33	778	22.2	484	2	BF826136	MR2-HN003
34	777	22.2	575	2	BE588616	194198 BA
35	775	22.2	541	4	BM843047	K-EST0120
36	764	21.8	504	4	BM842397	K-EST0119
37	754	21.6	452	4	BM761623	K-EST0042
38	739	21.1	895	4	BG419535	602446234
39	738	21.1	406	4	BM764289	K-EST0045
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41	725	20.7	403	2	BF825801	MR2-HN003
C 42	725	20.7	421	2	BF825871	MR2-HN003
C 43	724.5	20.7	421	2	BF828838	MR2-HN003
C 44	721	20.6	405	2	BF828608	MR2-HN003
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ALIGNMENTS

RESULT 1
AK040457
LOCUS
DEFINITION
AK040457 2935 bp mRNA linear HTC 03-APR-2004
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A43009B21 product:T cell cytokine receptor, full
insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK040457
AK040457.1 GI:26087864
HTC; CAP trapper.
Mus musculus (house mouse)

REFERENCE

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

REFERENCE

2
10349636

REFERENCE

3
11042159

REFERENCE

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11042159

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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillarary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2935)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES
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Query Match: 49.59% Indels: 140
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US-10-088-950A-1 (1-636) x AK040457 (1-2935)

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 Qy 440 alProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyT 460
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 DEFINITION 602713647F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853963 5',
 mRNA sequence.
 ACCESSION BG756328

VERSION BG756328.1 GI:14066981
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 900)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-@email.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLC1700 row: n column: 12
 High quality sequence stop: 750.
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 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGG(G). Size-selected
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 ORIGIN
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 Pred. No.: 7,12e-97 Length: 900
 Score: 1376.00 Matches: 282
 Percent Similarity: 94.08% Conservative: 4
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 Query Match: 39.34% Indels: 9
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 Qy 300 AlaValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSer 319
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 Qy 320 AlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuVal 339
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CK000257 783 bp mRNA linear EST 26-NOV-2003
IMAGE:16368614 NIH_MGC_220 Homo sapiens CDNA clone
CK000257
CK000257.1 GI:38526291
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 783)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDAMI070 row: m column: 16
High quality sequence stop: 651.
Location/Qualifiers

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Site 2: NotI; Library is oligo-dT primed and directionally
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gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to RNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGGCAGGAG)3' and 5'd
(CCTCGTGGCG)3'. 3' linker sequence - GCGCCCTCAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(ATTAACCTCACTAAGGAG)3'. 5' End: T7 promoter primer 5'd
(ATATACGACTCACTAAGG)3'. Library was constructed in the
laboratory of M. Bento Soares. Average insert size 3-4kb
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1,36e-89 Length: 783
Score: 1281.50 Matches: 243
Percent Similarity: 96.81% Conservative: 0
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US-10-088-950A-1 (1-636) x CK000257 (1-783)
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Qy 454 LeuCysAlaGlnSerGlyThrSerProSerVal 464
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RESULT 4
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 BQ957232
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 942)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC 40"
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.35e-87 Length: 942
 Score: 1251.00 Matches: 243
 Percent Similarity: 93.61% Conservative: 6
 Best Local Similarity: 91.35% Mismatches: 11
 Query Match: 35.76% Indels: 7
 DB: 5 Gaps: 2

US-10-088-950A-1 (1-636) x BQ957232 (1-942)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLeuAlaLeuLeu 20
 Db 130 ATGGGGGAGGACAGGGGGCCCTTTCTGGCTGTGGCGCTGCCCAAGCTGGGGCTGCTG 189

Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
 Db 190 CCTCTGTTGTGGTGTCTTTCCAGCGGACGGTCCCCAGGCGAGCGCGGCCACTGCAG 249

Qy 41 CysTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
 Db 250 TGTCTACGAGATTGGACCTTTGGCGCACTTGAACCTGCTCGTGGGATTNCCTGGGTGACCTG 309

Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTrpArgSerAsnLysThrGlnThr 80
 Db 310 GGAGCCCCCTCCGAGTTTACACCTCCAGAGCCAAACTACCTTCCAAACAAACCCAGACT 369

Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
 Db 370 GTGGCAGTGGCAGCGCGAGCTGGTGGCCATTCTCGGGAACAGCTCACCATGTCT 429

Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120
 Db 430 GACAAACTCCTTGTCTGGGGCACTAAGGCAGGCGAGCTCTCTGGCCCCCGCTCTCGTG 489

Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
 Db 490 AACTAGAAACCCAAATGAAGCCAAAGCCCCCGCTGGGCGCTGACGTGGACTTTTTC 549

Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
 Db 550 GAGGATGACCCCTGGAGGCACTGTCCATTGGGCCCCACTACATGGCCATCTCATATA 609

Qy 161 ValLeuLeuCysGlnPheHisTrpArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
 Db 610 GTTCTGATCTGCCAGTTCCACTACCGAAGATGTGAGGAGCGGCTGGACCTGCTGGAA 669

Qy 181 ProGluLeuLysThrLeuProLeuThrProValGluIleGlnAspLeuGluAlaThr 200
 Db 670 CCGAGCTGAAACCACTACCCCTGACCCCTGTGTGAGAC-CAAGATTGGAACTAGCCACT 728

Qy 201 GlyTrpLysValTrpGlyArgCysArgMetGluLysGluGluAspLeuTrp-GlyGluTr 220
 Db 729 GGCTACAAAGTGTATGGCCGCTGCGGATGGAGAAAGAGATTGTGGGGCGAGGTG 788

Qy 220 pSerProIleLeuSerPheGlnThrProProSerAlaProLysAspVal---TrpValSe 239
 Db 789 GAGCCCAATTTGCTCCCTCCAGACACCGCTCTCTGCTCCAAAGATGTGGGGGGAATCAC 848

Qy 239 rGlyAsnLeuCysGlyThrPro-GlyGlyGluProLeu-LeuLeu-TrpLysAlaPr 258
 Db 849 GGAACCTCTGGGGGGAAGCCCTGAAAGAAAGGAACCTTTGGCTTCTTAATGGAAGGCC 908

258 O---GlyPro 260
 909 CAAAGGCCCT 918

RESULT 5
 BQ984779
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1 (bases 1 to 896)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.

BP984779 896 bp mRNA linear EST 23-JAN-2001
 602308006F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4399248 5',
 mRNA sequence.
 BP984779
 BP984779.1 GI:12387591
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Inyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCW10102 row: 1 column: 01 High quality sequence stop: 678.		354 AspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProGly 373 600 GATGGGCTCGAGTGGGACCCCTG-GAGAACTCACTGGGTCCGGCTTCCCTGGG 658 374 AsnLeuSerAlaLeu---LeuProGlyAsnPheThrValGlyValProTyrArgIleThr 392 659 AAACCTCGAGTTGCTCTGTTACAAACGGCATTTTCACTGTCGGGGTCCCTATCGAATCACT 718 393 ValThrAlaValSerAlaSerGly-----LeuAlaSerAlaSerSer----- 406 719 GTGAACCGGAGCTCTGCTTCAGCTTGGCCCTCATCTCCGCTGGGGGTCTACGGGGTT 778 407 -----ValTrpGlyPheArgGluGluLeuAlaProLeuValGly 419 779 TTCCCCCTTGTGGGCACACCTTTGGGGATTGAGA-----ATGGCTCTGGAGACCCG 832 420 ProThrLeuTrpArgLeuGlnAspAlaProProGlyThr-----ProAlaIleAla 436 833 CCTATGTGTGG-----GGACGGCTCCGGGCGATTGGCGCTCCCCACATCGTG 893 437 TrpGly 438 884 TGGGG 889	
FEATURES source		RESULT 6 BO919454 911 bp mRNA linear EST 20-AUG-2002 LOCUS AGENCOURT 8822053 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6381506 5', mRNA sequence. ACCESSION BO919454 VERSION BO919454.1 GI:22334152 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 911) NIH-MGC http://mgi.nci.nih.gov/. AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Email: cgabbs-remail.nih.gov Tissue Procurement: DCTD/BTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2571 row: n column: 03 High quality sequence stop: 619. Location/Qualifiers 1. .911 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6381506" /tissue_type="carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 40" /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
ORIGIN		Alignment Scores: Pred. No.: 3,01e-83 Length: 911 Score: 1201.50 Matches: 245	

Percent Similarity: 90.51% Conservative: 3
 Best Local Similarity: 89.42% Mismatches: 10
 Query Match: 34.17 Indels: 17
 DB: 5 Gaps: 3

US-10-088-950A-1 (1-636) x BQ919454 (1-911)

Qy	1	MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
Db	107	ATGCGGGGAGGAGGGGGCCCTTTCCTGGCTGTGGCGCTGCCAAGCTGGCGCTGCTG	166
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
Db	167	CCTCTGTGTGGTGCTTTTTCAGCGGACGCGTCCCGAGGAGGCGCGGCGCACTGCGAC	226
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	227	TGCTACGAGATTGGACCCCTTGGGCGACTTGAACCTGCTGTGGAGGCTCTTGGGACCTG	286
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	287	GGAGCCCCCTCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCACAAAACCCAGACT	346
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	347	GTGGCAGTGTGGACGCGGAGGAGCTGGGTGGCCATTCTCTCGGGAACAGCTCACCATGCT	406
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
Db	407	GACAAACTCTTGTCTGGGCACTAAGGCAGGCCAGCCCTCTCTGGCCCCCGCTCTCTGG	466
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	467	AACCTAGAAACCCAAATGAAGCCAAACGCCCCCGCTGGGCCCTGACGTGGACTTTTCC	526
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	527	GAGGATGACCCCTGGAGGCCACTGCTCATTTGGGCCCCACCTACATGGCCATCTCATANA	586
Qy	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
Db	587	GTTCTGATCTGCCAGTTCACCTACCGAAGATGTACGAGGGCGGCTGGAACCTGCTGGAA	646
Qy	181	ProGluLeuLysThrIleProLeu-ThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	647	CCGAGCTGAAGACATACCCCTGGACCCCTGGTGGATCCAGATTTGGAGCTAGCCAC	706
Qy	200	rGlyTyrLysValTyrGly--ArgCysArgMetGluLysGluGluAspLeuTrp-GlyGly	219
Db	707	TGGCTACAAAGTGTATGGNCCGCTCGCGATGGAGAAAGAAAGATTTGTGGGGCGGA	766
Qy	219	uTrp-SerProIleuSer-PheGlnThrPro-ProSerAla-ProLysaspVal-Trp	237
Db	767	GTGGAACCCCATTTGTGCCCTTCAGACACCGGCTTCTGCTCCAAAGATGTGTGG	826
Qy	238	Val---SerGlyAsn---LeuCysGlyThrProGlyGlyGluGlu-----	250
Db	827	GTTATCCAGGGAACNTCTGTGGGAACCCCTT-GGGGAGGAAAGGGAAACCTTTT	885
Qy	251	ProLeuLeuLeuTrpLysAlaPro	258
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RESULT 7
 BF035293
 LOCUS 601457184P1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860781.5',
 DEFINITION mRNA sequence.
 ACCESSION BF035293
 VERSION BF035293.1 GI:10743020
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 681)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9596 row: g column: 22
High quality sequence start: 25
High quality sequence stop: 678.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

ORIGIN

Alignment Scores:		
Pred. No.:	5, 02e-81	Length:
Score:	1,70.50	Matches:
Percent Similarity:	95.15%	Conservative:
Best Local Similarity:	94.71%	Mismatches:
Query Match:	33.46%	Indels:
DB:	2	Gaps:

US-10-088-950A-1 (1-636) x BF035293 (1-681)

131	ProArgLeuGlyPro---AspValAspPheSerGluAspAspProLeuGluAlaThrVal	149
1	CCCCGGTCTGGGTCCCTGACTGTGGACTTTTCCGAGGATGACCCCTGGAGGCCACTGTC	60
150	HistTropAlaProProThrTTPProSerHisIysValLeuIleCysGlnPheHisTyr-Ar	169
61	CATTGGGGCCCCACCTACATGGCCACTCTCAATAAGTTCTGATCTGCCAGTTCCACTATCCG	120
169	gArgCysGlnGluAlaAlaTrpThrLeuLeuGluProGluLeuLysThrIleProLeuTh	189
121	AGATGTCCAGAGGGGGCTGGACCTCTGTGGAAACCGAGCTGAAGACCATACCCCTGAC	180
189	rProValGluIleGlnAspLeuGluLeuAlaThrGlyTyrLysValTyr-GlyArgCysAr	209
181	CCCTGTCTGAGATCCAGATTGGAGCTAGCCACTGGCTCAAAAGTGTATGGCCGCTGCCG	240
209	wMetGluLysGluGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPr	229
241	GATGGAGAAAGAGAGATTGTGGGCGAGTGGAGCCCATTTAGTCTCTCCAGACACC	300
229	oProSerHlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyCl	249
301	GCCTTCTGCTCCAAAAGATGTGTGGGTATCAGGGAACTCTGTGGGACGCCTGGAGGAGA	360
249	uGluProLeuLeuLeuTrpIysAlaProGlyProCysValGlnValSerTyrLysValTr	269
361	GSAACCTTGGCTTCTATGGAGGGCCCCAGGGCCCTCTGTGCGAGGTGAGCTACAAAGTCTGT	420
269	pPheTrpValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysCysSerLeuIle	289

RESULT 7
BF035293
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Db 421 GTTCTGGGTTGAGGTCGTGAGCTGAGTCCAGAGGAATTACCTGCTGCTCCTTAAT 480

Qy 289 eProSerGlyAlaGluTrpAlaArgValSerAlaValAlaThrSerTrpGluProLe 309

Db 481 TCCCAAGTGGGGAGTGGCCAGGAGTGTCCGCTGTCAACGCCACAAAGTGGAGCCTCT 540

Qy 309 uThrAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSe 329

Db 541 CAGCAAGCTCTCTTAGGTCGTGTTGATTCAGCCTCTGGCCCCCGTAGCGTGCCAGT 600

Qy 329 rSertleAlaGlySerThrGluLeuValThrTrpGlnProGlyProGlyGluProLe 349

Db 601 CAGCATCGTGGGACGACGACTACTGTGACCTGGCAACCGGGCCCTGGGGACCACT 660

Qy 349 uGluHisValValAspTrp 355

Db 661 CGAGCATGTAGTGGACTGG 679

RESULT 8

CV030371 620 bp mRNA linear EST 20-AUG-2004

LOCUS 9471 Full length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC028003, mRNA sequence.

DEFINITION CV030371

VERSION CV030371.1 GI:51488621

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,

Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,

Clingingsmith,T.R., Hartley,J.L., Esposito,D., Chao,D., Moore,T.,

Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,

Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.

Human ORFome Version 1.1: a Platform for Reverse Proteomics

Genome Res. (2004) In press

CONTACT: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

ORF Sequence tag (OST) of Gateway Entry construct. Each cloned ORF

results from a PCR reaction using an MGC full-length cDNA as

template DNA and ORF specific primers

PCR Primers

FORWARD: ATGCGGGAGGCGGGGCGC

BACKWARD: CAGGCCAGAACCTGTGGC

Insert length: 620 Std Error: 43.00

Plate: 11070 row: 06 column: H

Seq primer: ACTGGCGTCGTGTTACAAACGTGCTGACTGGGAAC

High quality sequence start: 99

High quality sequence stop: 619

FOLTA=NO. Location/Qualifiers

1..620

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="mixed"

/clone_lib="Full Length cDNA from the Mammalian Gene

Collection"

/notes="Vector: mixed; The ORFs were PCR amplified from the

MGC (Mammalian Gene Collection) as of April 2004 and

cloned by recombinational Gateway cloning into pDONR223

Donor vector. Reference : MGC (Mammalian Gene Collection)

Program Team, Generation and Initial Analysis of more than

15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,

2002, 99(26), 16899-16903"

ORIGIN

Alignment Scores:

Pred. No.: 1.54e-77 Length: 620

Score: 1125.00 Matches: 204

Percent Similarity: 99.51% Conservative: 1

Best Local Similarity: 99.03% Mismatches: 1

Query Match: 32.16% Indels: 0

DB: 7 Gaps: 0

US-10-088-950A-1 (1-636) x CV030371 (1-620)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20

Db 1 ATGCGGGAGGACAGGGGGCCCTTTCTGGCTGTGGCGCTGCCAAGTGGCGCTGCTG 60

Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40

Db 61 CCTCTGTGTGGTGTCTTTTCCAGCGACGCGTCCAGGCGCAGCGCGGCGCACTGCG 120

Qy 41 CysTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60

Db 121 TGCTACGGAGTTGGACCTTGGGGGACTTGAACGTCTCTGGTGGAGCCTCTTTGGGACCTG 180

Qy 61 GlyAlaProSerGlyLeuHisLeuGlnSerGlnLysTrpArgSerAsnLysThrGlnThr 80

Db 181 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAAACCCAGACT 240

Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaLeuProArgGluGlnLeuThrMetSer 100

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Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140

Db 361 AACCTAGAAACCCAAATGAAGCCAAACGCCGCCCGGCTGGGCGCTGACGTGGACTTTTCC 420

Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160

Db 421 GAGGATGACCCCTGGAGGCCACTGTCCATTGGGCCCCCACCCTAGATGCCATCTCATAAA 480

Qy 161 ValLeuLysCysGlnPheHisTrpArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180

Db 481 GTTCTGATCTGCCAGTTCACACTACCGAAGATGTGAGGAGCGGCTGACCCCTGCTGGAA 540

Qy 181 ProGluLeuLysThrIleProLeuThrProValGluLilleGlnAspLeuGluLeuAlaThr 200

Db 541 CCGGAGCTGAAGACCACTACCCCTGACCCCTGTGAGATCCAAGATTGAGGCTAGCCACT 600

Qy 201 GlyTrpLysValTrpGly 206

Db 601 GGCTANCAAGTGTATGGC 618

RESULT 9

BO927024

LOCUS BO927024

DEFINITION AGENCOURT_8779973 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6382739

5', mRNA sequence.

ACCESSION BO927024

VERSION BO927024.1 GI:22342055

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 950)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

FEATURES

source

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Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2575 row: a column: 12
High quality sequence stop: 469.
Location/Qualifiers
1. 950
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/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

```

ORIGIN

Alignment Scores:			
Pred. No.:	1,31e-75	Length:	950
Score:	1104.00	Matches:	235
Percent Similarity:	85.42%	Conservative:	11
Best Local Similarity:	81.60%	Mismatches:	28
Query Match:	31.56%	Indels:	15
DB:	5	Gaps:	3
US-10-088-950A-1 (1-636) x BQ927024 (1-950)			
QY	1	MetArgGlyGlyArgGlyValaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
Db	107	ATGCGGGAGGACGGGGGCCCTTCTTGCGTGTGGCGCGTGCCCAAGCTGGCGCTGCTG	166
QY	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
Db	167	CCTCTGTTGTGGGTGCTTTTCAGCGGACGGGTCCCGAGGGCAGCGCGGGCCACTGCAG	226
QY	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	227	TGCTACGGAGTTGGACCTTGGCGACATTGAACCTGCTGTGGGAGCCTCTTGGGGACCTG	286
QY	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	287	GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	346
QY	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	347	GTGGCAGTGGCAGCCGGACGGAGCTGGGTGGCGCCATTCTCGGGAACAGCTCACCATGTCT	406
QY	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrp-ProProValPheVa	120
Db	407	GACAAACTCTTTGTCTGGGGCACTAAGGCAGCGCCAGCCTCTCTGGCCCCCCCCGCTTCGT	466
QY	120	IleAsnLeuGluThrGlnMetLysProAsnAlaProArg-LeuGlyProAspValAspPheS	140
Db	467	GAACCTTAGAAACCCAAATTAAGCCAAACGCCGCCCGGGCTGGGGCCCTGACGTGGAC	526
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QY	160	LysValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaIleatTrpThrLeuLeu	179
Db	587	AAAGGTCTCATCTGCCAGTTTCACTACCGAAGATGGCAGGCGGCGCTGGGACCTGCTG	646

Qy	180	GluProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAla	199
Db	647	GAACCGACCTTGAGACCAATACCCCTGACCCCTGTTGAGAT-CAAGATTTGGAGCTAGCC	705
Qy	200	ThrGlyTyxLysValTyxGlyAtgCys-ArgMetGlu-LysGluGluAsp-LeuTrp-Gl	218
Db	706	ACTGGCTACCAACCGGATGGCCGCTGCCGATGGCAAAACAACATGATTTTGTGGGG	765
Qy	218	yGluTrpSerProIleLeuSer---PheGlnThrPro-ProSerAlaProLysAsp-Val	236
Db	766	CCAATGAACCCCAATTTTGGCCCTTCCAGACACCCCTTCTGCTCAAAAAAATGGG	825
Qy	237	TrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGlu-----ProLeuLeuLeu	254
Db	826	GGGGTATCCCGGGAACACCCCGGGTGCCCTCGAAGAGAAAGAAACCCCTTTGTTCTA	885
Qy	255	Tip-LysAlaPro--GlyProCysValGlnValSerTyxLysValTrpPheTrpValGl	273
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DEFINITION			
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ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.			
1 (bases 1 to 1028)			
NIH-MGC http://mgs.nci.nih.gov/ .			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cgabs-rc@mail.nih.gov			
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI			
CDNA Library Preparation: Rubin Laboratory			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
DNA sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LNL at:			
http://image.llnl.gov			
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Location/Qualifiers			
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into EcoRI/XhoI sites using the following 5' adaptor:			
GGCAGCAG(G). Library constructed by Ling Hong in the			
Laboratory of Gerald M. Rubin (University of California,			
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and			
Superscript II RT (Life Technologies). Note: this is a			
NIH MGC Library."			
ORIGIN			
Alignment Scores:			
Pred. No.:		7,05e-74	Length: 1028


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Db 116 CCTCTGTTGGTGTCTTCCAGGAGCGGTCCCGCAGT-ACAGGCGCTGGGCCACTG 174
Qy 40 GlnCysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAsp 59
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Qy 60 LeuGlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArg-SerAsnLysThrG1 79
Db 235 CTGGAGCCCTCCGAGTTACACTCCAGAGCCAAAGTACCTGTTCACAAACCCCA 294
Qy 79 nThrValAlaValAlaAla-GlyArgSerTrpValAlaLeuProArg-GluGlnLeuThr 98
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Qy 99 MetSerAspLysLeuLeuValTrpGlyThrLysAla-GlyGlnProLeuTrpProVa 118
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Db 415 CTTCGTGAACCTAGAAACCCAAATGAAGCCAAACCGCCCGGCTGGGGCCCTGACGTGGA 474
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Qy 217 rpGlyGluTrpSerPro 222
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DEFINITION mRNA sequence.
ACCESSION BG332437
VERSION BG332437.1 GI:13138875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 942)
NIH-MGC http://imgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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            /vector="pOTB7; Site 1: XhoI; Site 2:
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            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
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ORIGIN
Alignment Scores:
Pred. No.:      6,01e-72      Length:      942
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Percent Similarity: 92.86%    Conservative: 1
Best Local Similarity: 92.44%  Mismatches: 13
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Qy 437 TrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAla 456
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Qy 477 LeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGly 496
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Qy 497 GlnGlyProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLys 516
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found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stop: 435.

FEATURES

Location/Qualifiers

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Site 2: NotI; Library is oligo-dT primed and directionally

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primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated with

EcoR I adaptor, digested with Not I and then cloned

directionally into pYX-Asc vector. Average insert size

0.5-1kb. Adaptors 5'(AATTCGGCAGG)3' and 5'(

CCTCGGCG)3'. 3' linker sequence - GCGCCGCTGAGAGCC T18.

Sequencing primers 3' end: T3 promoter primer 5'd

(ATTACCCCTCACTAAGGGA)3'. 5' End: T7 promoter primer 5'd

(TTATACGACTACTATAGG)3'. Library was constructed in the

laboratory of M. Bento Soares. Average insert size 3-4kb

Note: this is a NIH_MGC Library."

ORIGIN

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US-10-088-950A-1 (1-636) x CF785854 (1-803)

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 570)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. Tissue Procurement: Louis M.
 Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html
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 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40

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Db      115  CCTCTGTTGGGGTGTCTTTCCAGCGGACGCGCTCCAGGGCAGCGCCGGGCCACTGCAG 174
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QY      81  ValAlaValAlaAlaGlyArgSerTyrValAlaIleProArgGluGlnLeuThrMetSer 100
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QY      101  AspLysLeuLeuValTyrGlyThrLysAlaGlyGlnProLeuTyrProValPheVal 120
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QY      121  AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
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QY      141  GluAspProLeuGluAlaThrValHisTyrAlaProProThrTyrProSerHisLys 160
Db      475  GAGGATGACCCCTGGAGGCCACTGTCCATTGGGCCCCACCTACATGGGCATCTCATAAA 534
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Search completed: February 23, 2005, 08:54:03
 Job time : 5431 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2005, 01:09:57 ; Search time 137 Seconds
(without alignments)
1519.163 Million cell updates/sec

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Perfect score: 3498
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3498	100.0	636	16	US-10-755-889-164 Sequence 164, App
4	3494	99.9	636	10	US-09-791-497-14 Sequence 14, Appl
5	3494	99.9	636	13	US-10-000-776-12 Sequence 12, Appl
6	3494	99.9	636	16	US-10-777-790-12 Sequence 12, Appl
7	380	10.9	862	10	US-09-853-180-5 Sequence 5, Appli
8	331	9.5	836	15	US-10-398-666-12 Sequence 12, Appl
9	297.5	8.5	836	16	US-09-972-708-9 Sequence 9, Appli
10	297.5	8.5	836	16	US-10-659-295-34 Sequence 34, Appl
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29	217.5	6.2	951	9	US-09-935-868-9	Sequence 9, Appli
30	217.5	6.2	951	14	US-10-287-035-9	Sequence 9, Appli
31	217.5	6.2	951	14	US-10-282-162-9	Sequence 9, Appli
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36	207	5.9	662	10	US-09-892-949-54	Sequence 54, Appl
37	207	5.9	662	14	US-10-006-265-17	Sequence 17, Appl
38	207	5.9	662	15	US-10-351-157-5	Sequence 5, Appli
39	207	5.9	662	15	US-10-352-554-5	Sequence 5, Appli
40	207	5.9	662	16	US-10-772-531-54	Sequence 54, Appl
41	207	5.9	662	16	US-10-715-667-15	Sequence 15, Appl
42	207	5.9	732	10	US-09-892-949-2	Sequence 2, Appli
43	207	5.9	732	15	US-10-351-157-111	Sequence 111, App
44	207	5.9	732	16	US-10-772-531-2	Sequence 2, Appli
45	206.5	5.9	1097	10	US-09-972-708-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-351-157-9
; Sequence 9, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-157-9

Query Match 100.0%; Score 3498; DB 15; Length 636;
Best Local Similarity 100.0%; Pred. No. 1e-256;

	Matches	636;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MRGRGAPFWLWPLKLLALLP	LFWLQRT	POGSAGP	QC	YGVG	PLGDLNCS	WEPLGDL	60	
Db	1	MRGRGAPFWLWPLKLLALLP	LFWLQRT	POGSAGP	QC	YGVG	PLGDLNCS	WEPLGDL	60	
Qy	61	GAPSELHLSQKYBSNKTOT	VANAAGRSWAI	PREQLT	MSDKILVWG	TKAGQPLW	PVFV	120		
Db	61	GAPSELHLSQKYBSNKTOT	VANAAGRSWAI	PREQLT	MSDKILVWG	TKAGQPLW	PVFV	120		
Qy	121	NLETQMKPNAPRLGPDVD	FSEDDPLEATVHWAP	PTWPSHKVLI	COFHYYRR	COEA	AAWTLLE	180		
Db	121	NLETQMKPNAPRLGPDVD	FSEDDPLEATVHWAP	PTWPSHKVLI	COFHYYRR	COEA	AAWTLLE	180		
Qy	181	PELXTIPLTPVEI	QDLLELATYKYVGR	CRMEKED	LGWESP	ILS	FOTPPSAPKDV	VWSG	240	
Db	181	PELXTIPLTPVEI	QDLLELATYKYVGR	CRMEKED	LGWESP	ILS	FOTPPSAPKDV	VWSG	240	
Qy	241	NLCGTPGGEERPLLWKA	PGPCVQYSKYVFW	WGREGRELS	PEGITCCCSLI	PSGAS	WARVSA	300		
Db	241	NLCGTPGGEERPLLWKA	PGPCVQYSKYVFW	WGREGRELS	PEGITCCCSLI	PSGAS	WARVSA	300		
Qy	301	VNATSWPELTNLSLVCLDS	SASAPRSVAVSS	IAGSTELLVT	WQPGEP	PLEHVVD	WARDGD	360		
Db	301	VNATSWPELTNLSLVCLDS	SASAPRSVAVSS	IAGSTELLVT	WQPGEP	PLEHVVD	WARDGD	360		
Qy	361	PLEKLNWVRPLPGNLS	ALLPQNFTVGP	PYRITVTAV	SASGLAS	SSVWGM	FREELAPLVGP	420		
Db	361	PLEKLNWVRPLPGNLS	ALLPQNFTVGP	PYRITVTAV	SASGLAS	SSVWGM	FREELAPLVGP	420		
Qy	421	TLWRLQADPGCTPAI	ANGVEPRHQLRGHL	THYTLCA	QSGTSPS	CMNVSGNT	QSVTLPLDL	480		
Db	421	TLWRLQADPGCTPAI	ANGVEPRHQLRGHL	THYTLCA	QSGTSPS	CMNVSGNT	QSVTLPLDL	480		
Qy	481	PWGCELWVTASTI	AGOPPGPIRLRLHLP	DNLTNRKVL	PGILFLWGL	PLGCGLS	LA	TS	540	
Db	481	PWGCELWVTASTI	AGOPPGPIRLRLHLP	DNLTNRKVL	PGILFLWGL	PLGCGLS	LA	TS	540	
Qy	541	RCYHLRHKVLPRW	WEKVPDPANSSSG	OPHMEQVPEA	QPLGDL	PLILEVEE	MEPPPV	MESS	600	
Db	541	RCYHLRHKVLPRW	WEKVPDPANSSSG	OPHMEQVPEA	QPLGDL	PLILEVEE	MEPPPV	MESS	600	
Qy	601	QPAQATAPLDSGYEKH	FLPTPEELGL	GLPPRPQVLA	636					
Db	601	QPAQATAPLDSGYEKH	FLPTPEELGL	GLPPRPQVLA	636					

RESULT 2.

US-10-352-554-9
; Sequence 9, Application US/10352554
; Publication No. US20030224487A1

GENERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

APPLICANT: Kuijper, Joseph L.

APPLICANT: Dasovich, Maria M.

APPLICANT: Grant, Francis J.

APPLICANT: Hammond, Angela K.

APPLICANT: Novak, Julia E.

APPLICANT: Gross, Jane A.
APPLICANT: Dillon, Stacey R.
TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
FILE REFERENCE: 02-01

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/ FILE REFERENCE: 02-01
/ CURRENT APPLICATION NUMBER: US/10/352,554
/ CURRENT FILING DATE: 2003-01-21
/ PRIOR APPLICATION NUMBER: US 60/350,325
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/375,323
/ PRIOR FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: US 60/435,315
/ PRIOR FILING DATE: 2002-12-19

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; LENGTH: 636
;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-352-554-9

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RESULT 3

RESULT 3
US-10-755-889-164
; Sequence 164, Application US/10755889
: Publication No. US20040171823A1

```

; GENERAL INFORMATION:
;
; APPLICANT: Bristol-Myers Squibb Company
;
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
;
; TITLE OF INVENTION: PATHWAY
;
; PUBLICATION NO.: 088000107130252

```

```

1 TITLE OF INVENTION: 2 FPHWAI
2
3 FILE REFERENCE: D0284 NP
4
5 CURRENT APPLICATION NUMBER: US/10/755,889
6
7 CURRENT FILING DATE: 2004-01-13
8
9 PRIORITY APPLICATION NUMBER: U.S. 60/440,068
10
11 PRIORITY FILING DATE: 2003-01-14
12
13 PRIORITY APPLICATION NUMBER: U.S. 60/459,757
14
15 PRIORITY FILING DATE: 2003-05-12
16
17 NUMBER OF SEQ ID NOS: 823
18

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-164

Query Match      100.0%; Score 3498; DB 16; Length 636;
Best Local Similarity 100.0%; Pred. No. 1e-256;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGRGAPFWLWPLPKLALLPLWVLFQRTPOGSAGPLOCYGVGPGLDNCNCSWEPLGDL 60
Db 1 MRGRGAPFWLWPLPKLALLPLWVLFQRTPOGSAGPLOCYGVGPGLDNCNCSWEPLGDL 60
Qy 61 GASELHLOSKQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Db 61 GASELHLOSKQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRCQEAATLLE 180
Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRCQEAATLLE 180
Qy 181 PELKTIPLTPVEIQDLATGYKYGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Db 181 PELKTIPLTPVEIQDLATGYKYGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Qy 241 NLGCTPGGEBPLLWKAPGCVQVSYKWFVWVGRELSPGITCCCSLIIPSGAEWARVSA 300
Db 241 NLGCTPGGEBPLLWKAPGCVQVSYKWFVWVGRELSPGITCCCSLIIPSGAEWARVSA 300
Qy 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHHVVDWARDGD 360
Db 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHHVVDWARDGD 360
Qy 361 PLEKLNWVRLPPGNLSALLPGNFTVGPYRITTVAVSASGLASASSVWGFEELAPLVGP 420
Db 361 PLEKLNWVRLPPGNLSALLPGNFTVGPYRITTVAVSASGLASASSVWGFEELAPLVGP 420
Qy 421 TMLRLQDAPGTPAIANGVEPRHQLRGHLTHYTLCAQSGTSPSPVCMNVSGNTQSVTLPLD 480
Db 421 TMLRLQDAPGTPAIANGVEPRHQLRGHLTHYTLCAQSGTSPSPVCMNVSGNTQSVTLPLD 480
Qy 481 PWGCELVWTASTIAGQGGPPIRLHLPLNTLRWKLPGILFLWGLFLGCGLSLATSG 540
Db 481 PWGCELVWTASTIAGQGGPPIRLHLPLNTLRWKLPGILFLWGLFLGCGLSLATSG 540
Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Db 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 4
US-09-791-497-14
; Sequence 14, Application US/09791497
; Publication No. US20030008343A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Pflianz, Stefan
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
; FILE REFERENCE: DX01040K2
; CURRENT APPLICATION NUMBER: US/09791,497
; CURRENT FILING DATE: 2001-02-22
; PRIOR FILING DATE: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-497-14

Query Match      99.9%; Score 3494; DB 10; Length 636;
Best Local Similarity 99.8%; Pred. No. 2e-256;
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRGRGAPFWLWPLPKLALLPLWVLFQRTPOGSAGPLOCYGVGPGLDNCNCSWEPLGDL 60
Db 1 MRGRGAPFWLWPLPKLALLPLWVLFQRTPOGSAGPLOCYGVGPGLDNCNCSWEPLGDL 60
Qy 61 GASELHLOSKQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Db 61 GASELHLOSKQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRCQEAATLLE 180
Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRCQEAATLLE 180
Qy 181 PELKTIPLTPVEIQDLATGYKYGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Db 181 PELKTIPLTPVEIQDLATGYKYGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Qy 241 NLGCTPGGEBPLLWKAPGCVQVSYKWFVWVGRELSPGITCCCSLIIPSGAEWARVSA 300
Db 241 NLGCTPGGEBPLLWKAPGCVQVSYKWFVWVGRELSPGITCCCSLIIPSGAEWARVSA 300
Qy 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHHVVDWARDGD 360
Db 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHHVVDWARDGD 360
Qy 361 PLEKLNWVRLPPGNLSALLPGNFTVGPYRITTVAVSASGLASASSVWGFEELAPLVGP 420
Db 361 PLEKLNWVRLPPGNLSALLPGNFTVGPYRITTVAVSASGLASASSVWGFEELAPLVGP 420
Qy 421 TMLRLQDAPGTPAIANGVEPRHQLRGHLTHYTLCAQSGTSPSPVCMNVSGNTQSVTLPLD 480
Db 421 TMLRLQDAPGTPAIANGVEPRHQLRGHLTHYTLCAQSGTSPSPVCMNVSGNTQSVTLPLD 480
Qy 481 PWGCELVWTASTIAGQGGPPIRLHLPLNTLRWKLPGILFLWGLFLGCGLSLATSG 540
Db 481 PWGCELVWTASTIAGQGGPPIRLHLPLNTLRWKLPGILFLWGLFLGCGLSLATSG 540
Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Db 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 5
US-10-000-776-12
; Sequence 12, Application US/10000776
; Publication No. US20020164609A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pflianz, Stefan K.-H.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, Jose F.
; APPLICANT: Rennick, Donna
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX01040K3
; CURRENT APPLICATION NUMBER: US/10/000,776
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
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; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2433)..(2433)
; OTHER INFORMATION: Unidentified base.
US-10-000-776-12

Query Match 99.9%; Score 3494; DB 13; Length 636;
Best Local Similarity 99.8%; Pred. No. 2e-256;
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRGGRGAPFWLWPKLALLPFWLWVLFQRTTRQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
DB 1 MRGGRGAPFWLWPKLALLPFWLWVLFQRTTRQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
QY 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLWPPVVF 120
DB 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLWPPVVF 120
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180
DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180
QY 181 PELKTIPLTPVEIQLELATGKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
DB 181 PELKTIPLTPVEIQLELATGKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
QY 241 NLCGTPGGEPELWPKAPGCPQVQSYKVFVWVGRELSPGEGITCCCSLIPSGAEWARVSA 300
DB 241 NLCGTPGGEPELWPKAPGCPQVQSYKVFVWVGRELSPGEGITCCCSLIPSGAEWARVSA 300
QY 301 VNATSWEPITNLSVCLDSASAPRSVAVSSVSSVSSVSSVSSVSSVSSVSSVSSVSSVSS 360
DB 301 VNATSWEPITNLSVCLDSASAPRSVAVSSVSSVSSVSSVSSVSSVSSVSSVSSVSSVSS 360
QY 361 PLEKLNWVRLPFGNLSALLPGNFTVGVYRITVTVAVSAGSLASVSSVWGFEELAPLVGP 420
DB 361 PLEKLNWVRLPFGNLSALLPGNFTVGVYRITVTVAVSAGSLASVSSVWGFEELAPLVGP 420
QY 421 TLWRLQDAPPGTPTAIWGEVPRHQLRGHLTHYTLCAQSGTSPVCMVNSGNTQSVTLTDL 480
DB 421 TLWRLQDAPPGTPTAIWGEVPRHQLRGHLTHYTLCAQSGTSPVCMVNSGNTQSVTLTDL 480
QY 481 PWGPCELWVTASTIAGQGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
DB 481 PWGPCELWVTASTIAGQGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
QY 541 RCYHLRHKVLPWWVEKVPDPANSSGGPHMEQVPEAOPGLDPLILEVEEMPPPPVMESS 600
DB 541 RCYHLRHKVLPWWVEKVPDPANSSGGPHMEQVPEAOPGLDPLILEVEEMPPPPVMESS 600
QY 601 QPAQATAPLDSGYEKHFLTPPELGLGPPRPQVLA 636
DB 601 QPAQATAPLDSGYEKHFLTPPELGLGPPRPQVLA 636

RESULT 6

US-10-777-790-12
; Sequence 12, Application US/1077790
; Publication No. US20040198955A1
; GENERAL INFORMATION:

; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pflanz, Stefan K.-H.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, Jose F.
; APPLICANT: Rennick, Donna
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX01040K3
; CURRENT APPLICATION NUMBER: US/10/777,790
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/10/000,776
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2433)..(2433)
; OTHER INFORMATION: Unidentified base.
US-10-777-790-12

Query Match 99.9%; Score 3494; DB 16; Length 636;
Best Local Similarity 99.8%; Pred. No. 2e-256;
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPKLALLPFWLWVLFQRTTRQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
DB 1 MRGGRGAPFWLWPKLALLPFWLWVLFQRTTRQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
QY 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLWPPVVF 120
DB 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLWPPVVF 120
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180
DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180
QY 181 PELKTIPLTPVEIQLELATGKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
DB 181 PELKTIPLTPVEIQLELATGKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
QY 241 NLCGTPGGEPELWPKAPGCPQVQSYKVFVWVGRELSPGEGITCCCSLIPSGAEWARVSA 300
DB 241 NLCGTPGGEPELWPKAPGCPQVQSYKVFVWVGRELSPGEGITCCCSLIPSGAEWARVSA 300
QY 301 VNATSWEPITNLSVCLDSASAPRSVAVSSVSSVSSVSSVSSVSSVSSVSSVSSVSSVSS 360
DB 301 VNATSWEPITNLSVCLDSASAPRSVAVSSVSSVSSVSSVSSVSSVSSVSSVSSVSSVSS 360
QY 361 PLEKLNWVRLPFGNLSALLPGNFTVGVYRITVTVAVSAGSLASVSSVWGFEELAPLVGP 420
DB 361 PLEKLNWVRLPFGNLSALLPGNFTVGVYRITVTVAVSAGSLASVSSVWGFEELAPLVGP 420
QY 421 TLWRLQDAPPGTPTAIWGEVPRHQLRGHLTHYTLCAQSGTSPVCMVNSGNTQSVTLTDL 480
DB 421 TLWRLQDAPPGTPTAIWGEVPRHQLRGHLTHYTLCAQSGTSPVCMVNSGNTQSVTLTDL 480
QY 481 PWGPCELWVTASTIAGQGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
DB 481 PWGPCELWVTASTIAGQGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540

QY 541 RCYHLRHKVLRWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEEMEPVPVMESS 600
Db 541 RCYHLRHKVLRWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEEMEPVPVMESS 600
QY 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVPPQVLA 636
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVPPQVLA 636
RESULT 7
US-09-853-180-5
; Sequence 5, Application US/09853180
; Publication No. US20030017617A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madaline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/09/853,180
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-180-5
Query Match 10.9%; Score 380; DB 10; Length 862;
Best Local Similarity 25.3%; Pred. No. 6.2e-20;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;
QY 31 RPOGSAGPLOCYGVPLGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71
Db 126 QPQN-----LSCIQEGQGTACTWGERGRDTHLYTEYTLQSLGPKNLTWQKQCKDIYCDYL 181
QY 72 -----KYRSNKTQV-AVAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPVPVFN 121
Db 182 DFGINLTPESPESNFTAKTAVNSLGSSSSLP-STFTFLDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVFEEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWLTLEP 181
Db 232 IKQ-KASVR-----CTLYWR-----DEGLVLLNLRYPNSRLNM----- 259
QY 182 ELKTIPLTPV-----EIQDLELATGYKYGRCRMEKEEDLWGEWSPILSFQTP---PSAPK 234
Db 270 ----VNVTKAKGRHDLDDLKPFTEYEFQISSKHLHYKGSWDSSESLSRAQTPEEPTGML 325
QY 235 DVWVSGNLCTPGCEEPILLWK-----APGCVQVSYKWFVWVGRELSPE--GITCCC 286
Db 326 DVWYMKRHIDY-SRQQLISLFWKNLSVSEARGKILHYQVTLQELTGGKAMTQNTIGHTSWT 384
QY 287 SLIPSGAEWA-RYSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSVSIAGSTELLVTWOP 343
Db 385 TVIPRTGNWAVASAANSKSSULPTRINIMNLCAGLLAPQVANS-EGWDLNLTWQP 443
QY 344 ---GPGEPLEHVVDWAR---DGDPLEKLNVRLLPQGNLSALLPQNFVTPVYRITVAVS 397
Db 444 PRKDPASAVQEVYVWEWRELHPGGDTQVPLNLRGRPNVNSALISENIKSYICYEIRVVALS 503
QY 398 ASGLASASSVWGFREELAPLVGPTLWFLQDAPGTPPAIANGEVPRHQLRHLTHYLTC-- 455
Db 504 GD-QGGCSSILGNSKKHAPLSGPHINAITE-EKGSILISWNSIPVQBMQCLLHYRYWK 561
QY 456 -AOSGTSFSPVC---MNVSGMTQSVTLPLDLPWGPCELWVTASTIAGQPGPILRLHPDN 511
Db 562 ERDNSQFQICEIPYVSQNSHPINSIQ-PRVTYVLMWTALTATAGESHPQGNERE 619
QY 512 TLRWK--VLPFI---LFLWGLFLGCGLSLATSRCYHLRHKVL-----PRWVWEKVP 559

Db 620 KANWMAFVAPSICIAITIMVGIF-----STHYFOQKVFVLLAALRPQWCSEIP 667
QY 560 DPANSSSQPH-----MEQVPEAQPLGDLPLILEVEEMEPVPVMESSQPAQATA-----PLD 610
Db 668 DPANSTCAKYPITAEKTKQLPLDRLLIDWTPPE-----DPEPLVISEVLHVQVTPVFRHPPC 723
QY 611 SGYEKHFLLPTPEELGLLG-----PPRQVPL 635
Db 724 SNWPQ-----REKGIQGHQASEKDMHMSASSPPPPREAL 756
RESULT 8
US-10-398-666-12
; Sequence 12, Application US/10398666
; Publication No. US20040073021A1
; GENERAL INFORMATION:
; APPLICANT: BIOTECHNOLOGY RESEARCH AND DEVELOPMENT CORPORATION
; TITLE OF INVENTION: CLONING AND SEQUENCING OF THE PORCINE INTERLEUKIN-12
; FILE REFERENCE: 21419/92796
; CURRENT APPLICATION NUMBER: US/10/398,666
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 861
; TYPE: PRT
; ORGANISM: Porcine sp.
US-10-398-666-12
Query Match 9.5%; Score 331; DB 15; Length 861;
Best Local Similarity 25.0%; Pred. No. 3.2e-16;
Matches 164; Conservative 83; Mismatches 263; Indels 146; Gaps 36;
QY 31 RPOGSAGPLOCYGVPLGDLNCSWEPLGD-----LGAPSELHLQSQ---KYRSNKT 78
Db 126 QPQN-----VSCMQKGERGTVACSWDRGRDTHLYTAVTLQNLGPKNLTWQKQCSYDCSL 181
QY 79 QTVAAGRSWVAIPRE-----QLTMSDKLLVWGTKAGQPLPVPVFNLETQMKPNA 130
Db 182 DL-----GINLPPESPESSTYATQVAINSL---GTASS---FPCTFTLLDV-VRLPL 226
QY 131 PRLGPDVFEEDDPLEATVHWAPPTWPSH-KVLICQFHYRRQCEAAWLTLEPELKTPLT 189
Db 227 PW---DIRK---CVNASVSTCTLQWRDEGLVLLNLRYPVYRSRWNVN---ATWAKG 277
QY 190 PVEIQDLELATGYKYGRCRMEKEEDLWGEWSPILSFQTP---PSAPKDVWVSGNLCTGP 246
Db 278 RHDVLDLKPFTEYEFQISSKPHLQKGRWSWSLSRTQTPEKEPTGMLDVWYMKQHIDYK 337
QY 247 GGEPEPILLWK-----APGCVQVSYKVFVWVGRELSPE 280
Db 338 -RQIYLFWKNLSLSARGKILH--YQVTLQEVAGNATLQNTERNSTWT----- 386
QY 281 GITCCCSLIPSGAEW-ARYSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSVSIAGSTEL 337
Db 387 -----IPRTGIMWAAVASAANSKSSULPTRINIAIDLQAGLLAPQVANSANP-EGSDNL 437
QY 338 LVTW-QPGEPLEP---BHVVDWAR---DGDPLEKLNVRLLPQGNLSALLPQNFVTPVYRI 391
Db 438 LVKWTSPGEGATAVQEVYVWEWRELHRLGRGMQPPLSWLRSPPYNTSTLISDNIPKICYEI 497
QY 392 TYTAVASGLASASSVWGFREELAPLVGPTLWFLQDAPGTPPAIANGEVPRHQLRHLTH 451
Db 498 RVHALSGD-QGGCSSIRGDLKHKAPLSGPHINAISE-EKGSILISWDEIPQAQBMQCGILH 555
QY 452 YTLG---AOSGTSFSPVC---MNVSGMTQSVTLPLDLPWGPCELWVTASTIAGQPGPILR 505
Db 556 YRIYWERUSDQFQICEIPYVSQNSHPINSIQ-PRVTYVLMWTALTATAGESHPQGNERE 614
QY 506 LHLPDNTLRWK--VLPFI---LFLWGLFLGCGLSLATSRCYHLRHKVL-----PRWV 555

Db 615 FCL-QCKANWSTFVAPSICIAVITGVF-----SMRCFRQKVFVLLIALRPQWCS 663

QY 556 EKVPDPANSSSQPH-----MEQVPEAQPLGDLPLILEVEEMPPPPVMESSQPAQAT 606

Db 664 REIPDPANSTWAKKYPIVEEKKQLSLDRLADWPTE-----EPEPLVINEVLPOVT 715

RESULT 9

US-09-972-708-9

; Sequence 9, Application US/09972708

; Publication No. US20030059871A1

; GENERAL INFORMATION:

; APPLICANT: Immunex Corporation

; APPLICANT: Cosman, David J.

; APPLICANT: Mosley, Bruce A.

; APPLICANT: Bird, Timothy A.

; APPLICANT: DuBose, Robert F.

; APPLICANT: Wiley, Steven R.

; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2

; FILE REFERENCE: 3160-B

; CURRENT APPLICATION NUMBER: US/09/972, 708

; CURRENT FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 9

; LENGTH: 836

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-972-708-9

Query Match 8.5%; Score 297.5; DB 10; Length 836;

Best Local Similarity 22.8%; Pred. No. 1.1e-13;

Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;

QY 50 LNCSEPLGDLGAPSELHLSQSKYRSN-KTQTVAV-----AAGRSWVAIPRQLTMSDKL 103

Db 140 LICQWEPGPEHLPFTSFTLSKFSKRGNCQTQDSILDVCPKDGQSHCCIPRKHLLLYQNM 199

QY 104 LVW-----GFKAGQPLW-----PPVFVNLETQMKNPAPRLG-----PDVDF 139

Db 200 GIWVQAEALGTSMSPQLCLDPMVVKLEPPMLRTMDPSPEAAPQAGCLQCWEP----- 255

QY 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRRCQEAANTLLEPELKTIPLTVEIQDLEL 198

Db 256 -----WQPLGHINQK-----CELHKKPQGEASWALVGP-----LPLEALQVEL 294

QY 199 -----ATGKVVYGRCRMEKEEDLWGEWSPILSFQTPPSAPK---DVWVSGNLCGTPGGBE 250

Db 295 CGLLPATAYTLQIRCIWRPLPGHWSDWSPSLERLITRATERPTVRLDTW----- 341

QY 251 PLLLLKAPGPCVQSVYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSANVATSWEP-- 308

Db 342 ----WRQ-----RQDPRTVQLFWKVPLEEDSGRIQGY-VVSWRPSG 379

QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335

Db 380 QAGAILPLCNTTELCTFHLPSAEQAEVALVAYNSAGTSRPTPVFSESGRPALTRLHAMA 439

QY 336 ----ELLVTWQPGCPGEBLHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGV 388

Db 440 RDPHSLWGWEPNPNWPGQYVIEWGLGPPSASNSKNKTWRMEQNGRATGFLKKNIRPFQ 499

QY 389 YRITVTAVSAGSLASASSVWGFEELAPLVGPTLWRLQDAPGTPTAIANGVPRHLRQH 448

Db 500 YEIIIVTPLYQDTMGPSQHVYAYSQEAWPASHAPL-HLKHIQKTAQLEWVWPEPPELGKSP 558

QY 449 LTHYTLCAQSGTSPSCVMNVSGNTQSVTLFDLPWGPCELW-----VTA 491

Db 559 LTHYTIFTWNAQNQSFAILNASSRGFVLHGLE--PASLYHIHLMAASQAGATNSTVLT 616

QY 492 STIAGOGPGPIRLHLPLDNTLRWKLPGILFLWGLFLL---CGGLSLATSGRCVHLRKH 548

Db 617 MTLTPEGS-----ELHI-----ILGLFGLLLLLTCLCG-----TAWLCCSPNRK 655

QY 549 VLPRVWVEKVPDPANSSSG-----QPHMBQVP---EAQPLGDLPLILEVEEMPPPPVMMES 599

Db 656 ---NPLWPSVDDPAHSSILGSVNPITMEEDAQLPCLGTPPTIKTLVLEDEKCKVP-WES 711

QY 600 SOPAQATAPLDSGYEKHFLPTPEELGLL-GPPR 631

Db 712 HNSSETCG-----LPTLVQTVYVLQGDPR 734

RESULT 10

US-10-659-295-34

; Sequence 34, Application US/10659295

; Publication No. US20040141946A1

; GENERAL INFORMATION:

; APPLICANT: SCHNEIDER, ARMIN

; APPLICANT: SCHAEBITZ, WOLFF-RUEDIGER

; APPLICANT: KOLLMAR, RAINER

; APPLICANT: SCHWAB, STEFAN

; TITLE OF INVENTION: METHODS OF TREATING NEUROLOGICAL CONDITIONS WITH HEMATOPOIETIC GRC

; FILE REFERENCE: 229530US

; CURRENT APPLICATION NUMBER: US/10/659,295

; CURRENT FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US/10/331,755

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 34

; LENGTH: 836

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-659-295-34

Query Match 8.5%; Score 297.5; DB 16; Length 836;

Best Local Similarity 22.8%; Pred. No. 1.1e-13;

Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;

QY 50 LNCSEPLGDLGAPSELHLSQSKYRSN-KTQTVAV-----AAGRSWVAIPRQLTMSDKL 103

Db 140 LICQWEPGPEHLPFTSFTLSKFSKRGNCQTQDSILDVCPKDGQSHCCIPRKHLLLYQNM 199

QY 104 LVW-----GFKAGQPLW-----PPVFVNLETQMKNPAPRLG-----PDVDF 139

Db 200 GIWVQAEALGTSMSPQLCLDPMVVKLEPPMLRTMDPSPEAAPQAGCLQCWEP----- 255

QY 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRRCQEAANTLLEPELKTIPLTVEIQDLEL 198

Db 256 -----WQPLGHINQK-----CELHKKPQGEASWALVGP-----LPLEALQVEL 294

QY 199 -----ATGKVVYGRCRMEKEEDLWGEWSPILSFQTPPSAPK---DVWVSGNLCGTPGGBE 250

Db 295 CGLLPATAYTLQIRCIWRPLPGHWSDWSPSLERLITRATERPTVRLDTW----- 341

QY 251 PLLLLKAPGPCVQSVYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSANVATSWEP-- 308

Db 342 ----WRQ-----RQDPRTVQLFWKVPLEEDSGRIQGY-VVSWRPSG 379

QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335

Db 380 QAGAILPLCNTTELCTFHLPSAEQAEVALVAYNSAGTSRPTPVFSESGRPALTRLHAMA 439

QY 336 ----ELLVTWQPGCPGEBLHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGV 388

Db 440 RDPHSLWGWEPNPNWPGQYVIEWGLGPPSASNSKNKTWRMEQNGRATGFLKKNIRPFQ 499

QY 389 YRITVTAVSAGSLASASSVWGFEELAPLVGPTLWRLQDAPGTPTAIANGVPRHLRQH 448

Db 500 YEIIIVTPLYQDTMGPSQHVYAYSQEAWPASHAPL-HLKHIQKTAQLEWVWPEPPELGKSP 558

QY 449 LTHYTLCAQSGTSPSCVMNVSGNTQSVTLFDLPWGPCELW-----VTA 491

Db 559 LTHYTIFTWNAQNQSFAILNASSRGFVLHGLE--PASLYHIHLMAASQAGATNSTVLT 616


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QY      266 YKWFWVGVBRELSPEGITCCCSLIPSGAEWA-----RVSAVNAIATSWEPL 309
Db      465 YNI--AVVENAKPTESEHYC-----WVPALSTNLSDLQPYKIRITANNMWSGASP- 513
QY      310 TNSLVCLDSASAPRSVAVSIAAGSTELLVTMQPGPEPLEHVVDM-ARDGDPLEKLNVW 368
Db      514 ESLMVLSNDSHGHEVKETIKIGIDAFN--ISWEBPVGGDTMGVGVVDWCASHSQDQCDDJQM 571
QY      369 RLPPGNLSALLPG-NFTVGPYPYRITTVTAVSASGLAS-ASSVMWGPREELAPIUGPTLRWLQ 426
Db      572 NLGENTTTITSDDFKPGVRYNFRIFERSVEHKARLVEKGQGYTOELAPLVNPKV---- 627
QY      427 DAPPGET---AIANGEVPRHLRGHLTHYTICAOS-----GTSPSVCMVN 468
Db      628 EIPYSTNSSFVLRPDPYSDSFQAQFIKGYLYVVKSKEMOCNQCPWERTILLPDNSVLCKYDI 687
QY      469 SGN-TQSOTLPDL-PWGPCELWTVTASTIAGOPGPILRLHLDPNTLRWKVLPGLFLPWG 526
Db      688 NGSETKTTLTENLOPESLYEFVPTYTSAGPGNETTKVTPD--ARKSHMLQLLIPLMT 745
QY      527 LFLGCGSLATSCRCYHLRHKLVLPRWWKEK-----VDPANSS----- 565
Db      746 LCVL--LSIIIV--CYW-----KSQWKEKYCDPIENPKYSILSIKSNPHLINW 794
QY      566 -----SGQHMEQVPEAQPLGIDLPILEEBEPPPWNBSQP 602
Db      795 KDCIPDVLEINVINKAESKTCVGSGLHIEDVTKPPI--VP-TEKDSSGGVPCIFFNF 851
QY      603 AQATAPLDSDGEKHFL-----PTEEGLLGPP 630
Db      852 TYQSAFD SG--SHGLIPGPLXDTAHLQGLLAPP 883

RESULT 13
US-10-352-554-120
; Sequence 120, Application US/10352554
; Publication No. US20030224487A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Novak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
; FILE REFERENCE: 02-01
; CURRENT APPLICATION NUMBER: US/10/352,554
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIORITY FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/375,323
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/435,315
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 970
; TYPE: PRt
; ORGANISM: Mus musculus
US-10-352-554-120
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Db      306  TLTAENQLRKRSVN-----INFLNTHRVHPKAQO---DVTLLKIIGATKANMTWKVHS 354
QY      156  WPSHKVLLICOFHYRRQCEAAWTLLEPELTKTIPTPVEIQDELATGKYVGRCRMKEED 215
Db      355  HGNNYTLCCOVKLOYGE---VTHEHNVSVHMSANYLFSDDLDPDTKYKAFVRCASAHFW 410
QY      216  LWGEWSPILSFOTPPSAPK--DWVSGNLCGTPGGEPELILLWKAPGCVQ-----VS 265
Db      411  KMSDWTDQ-KEFSTPETAPSQALDWM--RQVWSENGRRIVTLFWK---PLLKSEQANGKIIS 464
QY      266  YKWFVWVGGRLESPGEGITCCSLIPSGAEWA-----RVSAVNATSWEPL 309
Db      465  YNT---VVENEAAPTSEHYC-----WAPALSTNLSDLQPYKIRITANNENGASP- 513
QY      310  TNLSQLCLDSASAPRSVAVSIIAGSTELLVTWOPGGEPELHVVDW-ARDGDPLEKLNWV 368
Db      514  ESLMWLNSDGHGHEVKEKTIKIGDAFN--ISWEPVSGDTMGVYVDWCAHSQDQRCDLQWK 571
QY      369  RLPFGNLSALLPG-NFTVGVPYRITVTAVSASGLAS-ASSWVGPRELAPLVGFTLWRLQ 426
Db      572  NLGENTTTTITSDDFKPGVRYNFRIFERSVEHAKARLVEKRGYTOELAPLVNPKV---- 627
QY      427  DAPGPGTP---AIWAGEVPRHQLAGHLTHYTLCAQS-----GTSFSPVCMNV 468
Db      628  EIPYSTPNSVFLWRKPDYDSDFQAGFNGYLVYVYSKEMQCNQPWERTLLPDNSVLCKYDI 687
QY      469  SGN-TQSVTLPLDL-PWGPCBLWYTASTIAGCGPPGPIRLHLPLDNTLRWKVLPGLIFLWG 526
Db      688  NGSETKTLTVENLOPESLYEFFVPTVTSAGPGNETFTKVTTPD--ARSHMLLQIILPMT 745
QY      527  LFLTLCGLSLATSGRCYHLRHKVLPRWWEK----VDPDANSS----- 565
Db      746  LCVL---LSIIV---CYW-----KSNQVKEKCPDIPNPKYSILSLIKKNPHLIMNV 794
QY      566  -----SGOPHMQVPEAOPLGDLPLILEVEEMPPPPVWESSQP 602
Db      795  KDCIPDVLVINKAEGSKTCVSGKLIHEDVTKPI--VP-TEKDSSGVPVPCIFFENF 851
QY      603  AQATAPLDSYEXHFL-----PTPEELGLLGPP 630
Db      852  TYDQSAFDSG--SHGLIPGLKDTAHLQGLLAPP 883

RESULT 14
US-10-659-295-35
; Sequence 35, Application US/10659295
; Publication No. US20040141946A1
; GENERAL INFORMATION:
; APPLICANT: SCHNEIDER, ARMIN
; APPLICANT: SCHABITZ, WOLP-RUEDIGER
; APPLICANT: KOLLMAR, RAINER
; APPLICANT: SCHWAB, STEFAN
; TITLE OF INVENTION: METHODS OF TREATING NEUROLOGICAL CONDITIONS WITH HEMATOPOIETIC GROWTH FACTORS
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: 229530US
; CURRENT APPLICATION NUMBER: US/10/659,295
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/10/331,755
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-659-295-35

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Db 123 PPASPSNLSCLMHLTNSLVQWEPGPEETHLPSTFILKSFRRADCOYQSGTIPDCVAKK 182
Qy 87 R-SWVAIPREQLTMSDKLLVW-----GTRAGQPLW--PPVFNLETKMPNAPRLGPD 136
Db 183 RQNNCSIPRKNLLLYQYNAIWQAEENMLGSSPKCLCLDPMDVVKLEPPML-QALDIGPD 241
Qy 137 VDFSEDDPLEATVHWAPTWFSHKVL--ICQFHYR-RCQEAATLL--EPBLKTIPLTPV 191
Db 242 V--VSHQGCILWLSWKP--WKPSEYMEQECBLRYQPLKGANWTLVFLHPSK-----DQF 293
Qy 192 EIQDLELATGKYVYRCRMEKEEDLWGEWSPILSFQTPPSAPK---DWWSGNLGCTPGG 248
Db 294 ELGLHQAPVYTLQMCIRIRSLPGFWSFGLQRLPTMKAPTIRLDTWCOKQL--DEGT 352
Qy 249 BEPLILWKAPGCVQVSKWFWF-----GRELSPGEGIT--CCSLIPSGAEWARV 298
Db 353 VSVQLFWK-PTPLQEDSQIOGYLLSWNSPDHQDQIHLNCTTQLSCTILFPSAQ----- 407
Qy 299 SAVNATSWEPITNLSVCLDSA--SAPRSV-----AVSSIAGSTS-----LLVTWQPG 344
Db 408 -----NVTLVAYNKAQTSPTTVPFLENEGPAVTGLHAMAQDLNTIWDWEAP 455
Qy 345 PGEPLHVVDWARDGDPLEK--LNMVRLPPGNLSA--LLPGNFTVGVYRITVAVSAGL 401
Db 456 SLLPGYLIIEWEMSPSYNSYSKSMITFPNGNITGILKONINPFQLYRITVAPLYGIV 515
Qy 402 ASASSVWGFREELAPLVGP-----TLWLQDAPPGTPAIANGVEPRHLRGLHLYT 453
Db 516 GPPVNVYTFAGERAPPAPHALHLKHVGTWQAQLEWVPEAPL--GMIP-----LTHYT 566
Qy 454 L-CAQSGT-SPSCVMVNGTQSVTLPLD--PWGPELWVTASTIAGO--GPEGPILRLHLP 509
Db 567 IFWADAGHSFSTLNIS--LHDFVLKHLSPASLYHVYLMATSRAGSTNSTGLTLRLTLD 624
Qy 510 DNTLRWKVLPGLFLWGLFLGCGLSLATSRCYHLRHKVLPWWWEKVPDPDANS----- 565
Db 625 SDL-----NIFGLICLVLLSTTCVTVWLCCKRRGKTS---FWSDDVPDPAAHSSLSW 673
Qy 566 -----SQQPHMQVPEAQP-----LGDLPLI---EVEEME 592
Db 674 LPTIMBETFPQPSFWDSSVPSITKITELEDKXPTWDSSESSNGSLPALVQAYVLQGD 733
Qy 593 PPPWESSQAQATAPLDSGYEKHFLPTPELG-----LLGPPRP 632
Db 734 PREISNQSPSRGTG--DQVLYGVLESPTSPTGVMQVIRSDTQPLLGPTP 783

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RESULT 15

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US-09-853-180-4
; Sequence 4, Application US/09853180
; Publication No. US20030017617A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madaline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/09/853,180
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-180-4

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Query Match 7.1%; Score 250; DB 10; Length 918;
 Best Local Similarity 20.5%; Pred. No. 4.9e-10;

```

Matches 133; Conservative 81; Mismatches 255; Indels 180; Gaps 22;
Qy 119 FVNLET-----OMKPNAPRLGPDVDRSEDDPLEATVHWAPPTW 156
Db 191 FVNIEVWEAENALGKVTSHINFDPVYKVKPNPPH-NLSVINSEELSSILKLTWTWPSI 249
Qy 157 PSHKVLICQFHYRCQBAAWTLLEPELKTIPLTPEIQDLELATGYKYVYRCRMEKEEDL 216
Db 250 KSVIILKYNQYRTKDASTWSQIPPEDTASTRSFTQDLKPFTEYVFRIRCMKEDGKG 309
Qy 217 WGEWSPI---LSFQTPPSAPKDVWVSGNLGCTPGGEEPLLWKAPGCVQVSKWFWG 273
Db 310 WSDMSEASGITVEDREDSKAPSFMYKIDPSHTQGYRTVQLVWKTLP-----FEAN 360
Qy 274 GRELSPEGITCCCSLIPSGAEWARVSAVNATSWEP-LTNLSL-----VCLDSASAPRSV 326
Db 361 GKILDYE-----VTLTRKSHLQNTVYVATKUTVNLNTDRLATL 400
Qy 327 AVSSIAGSTELLVTWQPGGPELHV-----VDWARDGDPLEK--LNMVRL 370
Db 401 TVRNLVGKSDAAVLTIIPACDFQATHPVMDLKAPKDNMLWVEMTTPRESVKKYILECVL 460
Qy 371 -----PPGNL-SALLPGNFTVGVYRITVAVSAGLSASSVWGFREELAPL 417
Db 461 SDKAPCITDQOEDGTVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPS 520
Qy 418 VGPTLWELQDAPPCTPAIANGVEPRHLRGLHLYTILCAOSGTSVSCVMVNGTQSVTL 477
Db 521 KGFTV-RTKKVGKNEAVLEWDQLPVDVQNGFIRNYTIFRTIIGNETAVNVDSSTHTYL 579
Qy 478 PDLFWGPELWVTASTIAGQPGPILRLHLP---DNTLRWKVLPGLFLWGLFLGCGL 534
Db 580 SSLTSDTLVWVMAAYTDEGKGDPFTFTTPKFAQGEIEAIVVPVCL-----APLLTLL 635
Qy 535 SLATSGRCYHLRHKVLPWWWEKVPDPANSSGQ--PH-----MEQVPEAQPLGDL 583
Db 636 GVLF---CFNKR-DLIKHIWPNVDPSPKSHIAQWSPTPPRHNFNSKQOMYSDGNFTDV 691
Qy 584 PILEVEEMEPPP-----VMESSQPA----- 603
Db 692 SVVEIENDKKPPEDLKSLLDFKKEKINTEGHSIGGSSCMSSSRPSISSDENESSQ 751
Qy 604 -----QATAPLDSGYEKHFLPT-----PEELGLL 627
Db 752 NTSSTVQYSTVHVHSGY-RHQVPSVQVFSRSESTQPLLDSEERPEDLQLV 799

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Search completed: February 19, 2005, 01:20:02
 Job time : 140 secs

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OM protein - protein search, using sw model

Run on: February 19, 2005, 01:06:55 ; Search time 43 Seconds
(without alignments)
1423.113 Million cell updates/sec

Title: US-10-088-950A-1
Perfect score: 3498
Sequence: 1 MRGGRGAPFWLPLPKALL.....FLTPBELGLGPPRPQVLA 636
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	2 JW0047	class I cyto kinase
2	298.5	8.5	783	2 JH0329	granulocyte colony
3	292	8.3	863	2 C3852	granulocyte colony
4	277	7.9	837	2 A34898	granulocyte colony
5	268.5	7.7	771	2 B38252	granulocyte colony
6	250	7.1	918	2 A36337	membrane glycoprot
7	248	7.1	917	2 I49699	glycoprotein 130 -
8	226.5	6.5	918	2 A44257	interleukin-6 sign
9	206.5	5.9	1097	2 S17308	leukemia inhibitor
10	206	5.9	1092	2 JX0312	differentiation-st
11	178	5.1	894	1 A41527	protein-tyrosine k
12	170	4.9	1711	1 A55148	protein-tyrosine-p
13	164.5	4.7	1185	2 T46428	hypothetical prote
14	162.5	4.6	1197	2 T30581	neural cell adhesi
15	159	4.5	1825	2 C88400	protein H19W22.1 {
16	159	4.5	1825	2 T32828	hypothetical prote
17	155	4.4	942	2 S23251	protein-tyrosine k
18	154.5	4.4	880	2 B53743	protein-tyrosine k
19	151	4.3	1274	2 S55050	cardiac myosin-bin
20	151	4.3	1914	2 T42635	tenascin Y precurs
21	150	4.3	888	2 S23085	uto protein - mous
22	150	4.3	1232	2 T43037	neural cell adhesi
23	147.5	4.2	800	1 S31575	interleukin-4 rece
24	147.5	4.2	1239	1 A32579	neuroglian - fruit
25	146	4.2	876	2 I49152	protein-tyrosine k
26	146	4.2	1691	1 D54689	protein-tyrosine-p
27	144	4.1	890	1 A53743	protein-tyrosine k
28	144	4.1	1894	2 C54689	protein-tyrosine-p
29	143.5	4.1	4135	2 T42629	tenascin-X - bovin

30	142.5	4.1	1898	2 S46216	leukocyte antigen-
31	142	4.1	880	1 JC4166	protein-tyrosine k
32	141.5	4.0	1907	2 S50893	protein-tyrosine-p
33	140.5	4.0	862	2 T46289	hypothetical prote
34	140.5	4.0	1344	2 T14316	rig-1 protein - mo
35	140.5	4.0	2302	2 T14328	protein-tyrosine-p
36	138.5	4.0	581	2 I45971	prolactin receptor
37	137	3.9	896	2 I56563	interleukin-3 rece
38	137	3.9	1257	1 A41060	neural cell adhesi
39	137	3.9	1259	2 A43425	Bravo/Nr-CAM cell
40	137	3.9	1268	1 A39640	neural cell adhesi
41	136	3.9	2944	2 A54849	collagen alpha 1(V
42	135.5	3.9	2222	2 T13924	adk protein - fru
43	135	3.9	3164	1 WMBEH6	UL36 protein - hum
44	134.5	3.8	1162	2 PC4184	leptin receptor, O
45	134.5	3.8	1742	2 S24600	projectin - fruit

ALIGNMENTS

RESULT 1

JW0047

class I cytokinase receptor precursor - human

N;Alternate names: WSX-1

C;Species: Homo sapiens (man)

C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004

C;Accession: JW0047

R;Sprecher, C.A.; Grant, P.J.; Baumgartner, J.W.; Preenell, S.R.; Schrader, S.K.; Yamagi

Biochem. Biophys. Res. Commun. 246, 82-90, 1998

A;Title: Cloning and characterization of a novel class I cytokine receptor.

A;Reference number: JW0047; MUID:98262921; PMID:9600072

A;Accession: JW0047

A;Molecule type: mRNA

A;Residues: 1-636<SPR>

A;Cross-references: UNIPROT:O60624; GB:AF053004; MID:g3153240; PIDN:AAC39755.1; PID:g315

A;Experimental source: brain

C;Genetics:

A;Map position: 19p13.11

C;Keywords: glycoprotein

F;1-32/Domain: signal sequence #status predicted <SIG>

F;515-540/Domain: transmembrane #status predicted <TM>

F;554-561/Domain: cytoplasmic #status predicted <CTP>

F;51,76,302,311,374,382,467/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 100.0%; Score 3498; DB 2; Length 636;

Best Local Similarity 100.0%; Pred. No. 5.8e-229; Mismatches 0; Indels 0; Gaps 0;

Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGGRGAPFWLPLPKALLPLLVLFQTRPQGSAGPLQCYGVGLDNLCSWEPLGDL 60

Db 1 MRGGRGAPFWLPLPKALLPLLVLFQTRPQGSAGPLQCYGVGLDNLCSWEPLGDL 60

Qy 61 GAPSELHLSQKQYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTVKAGQPLWPFV 120

Db 61 GAPSELHLSQKQYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTVKAGQPLWPFV 120

Qy 121 NLETKMKVAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHYRCCQEAATLLE 180

Db 121 NLETKMKVAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHYRCCQEAATLLE 180

Qy 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240

Db 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240

Qy 241 NLCGTGGEEPLLWLKAPGCVQVSYKVMFWVVGRELSPEGITCCCSLIPSGAEWARVSA 300

Db 241 NLCGTGGEEPLLWLKAPGCVQVSYKVMFWVVGRELSPEGITCCCSLIPSGAEWARVSA 300

Qy 301 VNATSWEPLTNLSLVCLDSASAPRSVAVSIAGSTILLVTWQPGCEPLEHVVDWARDGD 360

Db 301 VNATSWEPLTNLSLVCLDSASAPRSVAVSIAGSTILLVTWQPGCEPLEHVVDWARDGD 360

A;Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA44515.1; PID:9840817
 C;Genetics:
 A;Gene: gp130
 C;Keywords: glycoprotein
 F;134-314/Domain: cytokine receptor homology <CRS>

Query Match 7.1%; Score 248; DB 2; Length 917;
 Best Local Similarity 21.1%; Pred. No. 6e-09;
 Matches 140; Conservative 85; Mismatches 253; Indels 186; Gaps 27;
 QY 107 GTKAGQPLWPPVFNLETKM-PNAPRLG-----PDVDFSEDDPLEATVHAPP----- 154
 DB 177 GTSCWVSMPYIYNIEVWEAEN--LGKVSSESINFDVVDKVPKPT-----PPYNLSVTN 230
 QY 155 -----TWPSHKV-----LICQFHYRCQBAWTLLEPELKTITPLTVEIQDLELA 199
 DB 231 SEELSSILKLSWSSGLGLDLKSDIQRTKDASTWIOVPLEDTMSPRTSFTVQDLKPF 290
 QY 200 TGYKVGRCRMEKEEDLWGEWSPILS---FOTPPSAKDVWVSGNLCTGPGGEEPLLLWK 256
 DB 291 TEYVFRIRSKDQSGKYSWSEASGTTVEDRSPRPPEFWYKTNPSHGQYRSVRLWK 350
 QY 257 APGPCVOVSQYK-----WFMVGGRELSPE-----GITCC 285
 DB 351 AL-PLSEANGKILYEVILTQSKSVSQTYVTGTGLTNLTNDRYVASLAARNKVGKSA 409
 QY 286 CSL-IPSGAEWARYSAVNATSWELTNLSLVCLDSASAPRSVAVSSITAGSTELLVTWQP 344
 DB 410 AVLTIPSHVTAAYSVVNLKAF-PKDNL-----LWVEWTPP 444
 QY 345 PGEPLHVDWA---RDGDPLEKLNWRLPGNLSALLPGNFTVGVPIRITVAVSASGLA 402
 DB 445 PKPVSKYLECWLSENAPCVE-DWQGEDATVNRTHLRGLLESKCYIITVTPVPAATGP 503
 QY 403 SASSVWGFREELAPLVGPTLWELQDAPGTPAIAWGEVPRHQLRGLHLYTLCAQSGTSP 462
 DB 504 GSESLKAYLQQAAPRGTV-RTKVKGNEAVLAWDQIPVDDQNGFIRNYSISYRTSVGK 562
 QY 463 SVCNVSNGTQSVTLPLDPLMPGCPBLWVTAIAQGGPPGPILRLHLP---DNTLRWKVLP 519
 DB 563 EMVHVDSSTHTEYTLSSSDTLVWVMAAYTDEGGKDGPEFTTLPKPAQGHIEALVVP 622
 QY 520 GILPLWGLFLGCGLSLATSGRCHLHKVLPVWVWKEKVPDPANSSGQ---PH----- 570
 DB 623 VCL-----AFLTLTLLGVLF---CFNKR-DLIKKHWPVDPDSKSHIAQWSPHTPPRHNF 674
 QY 571 --MEQVPEAQPLGDLPILEVEEMEPPP-----VMS 599
 DB 675 NSKDMQYDGNFTDVSVVEIANNKPCPDLDKSVDLFKKVKVSTEGHSGIGSSCMSS 734
 QY 600 SQP-----AQATAP-----LDSGYEKHFLLPT-----PEE 623
 DB 735 SRPSISSNEENESAQSTASTVEYVTVHSGY-RHQVPSVQVFSRSESTQPLDSEERPED 793
 QY 624 LGLL 627
 DB 794 LQLV 797

RESULT 8
 A44257
 interleukin-6 signal transducing molecule gp130 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A44257
 R;Wang, Y.; Nesbitt, J.E.; Puentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A;Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
 A;Reference number: A44257; MUID:93052397; PMID:1427893
 A;Accession: A44257
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-918 <WAN>

A;Cross-references: UNIPROT:P40190
 A;Experimental source: liver
 A;Note: sequence extracted from NCBI backbone (NCBIP:118488)
 C;Keywords: transmembrane protein
 F;134-315/Domain: cytokine receptor homology <CRS>

Query Match 6.5%; Score 226.5; DB 2; Length 918;
 Best Local Similarity 20.2%; Pred. No. 1.7e-07;
 Matches 130; Conservative 84; Mismatches 271; Indels 157; Gaps 23;
 QY 105 VW-----GTKAGQPL-WPPVFNLETKMKNAPRLGPDVDFSEDDPLEATVHAPP 156
 DB 195 VWVEAENALGNVSESEINFDV-----DKVKPSPPH-NLSVTNSEELSSILKLAWSNGL 248
 QY 157 PSHKVLICQFHYRCQBAWTLLEPELKTITPLTVEIQDLELATGYKVGRCRMEKEEDL 216
 DB 249 DSILRLKSDIQRTKDASTWIOVPLEDTVSPRTSFTVQDLKPFTEYVFRIRSKENCKGY 308
 QY 217 WGEWSPILS---FOTPPSAKDVWVSGNLCTGPGGEEPLLLKAPGCPVQVSQYK----- 268
 DB 309 WSDWSEASGTTVEDRSPKAPSEFWYKVNANHPQYRSARLIWKT-PLSEANGKILDYEV 367
 QY 269 -----WFMVGGRELSPEGITCCSLIPSGAEWARYSAVNATSWELTNLSLVCLD 318
 DB 368 VLTQSKSVSQTYVTGTGLTN-----LTNRYVASLAARNVVGKSPATVLTIPGSH 419
 QY 319 SASAPRSVAVSSITAGSTELLVTWQPGGEPLEHW-----DWARDGDPLEK 364
 DB 420 FKASHPVVDLKAPKDNLLWVEWTP-PSKPVNKYILEWCVLSENSCPDPWQGEDGTNR 478
 QY 365 LNWVRLPPGNLSALLPGNFTVGVPIRITVAVSASGLASASSVWGFREELAPLVGPTLWR 424
 DB 479 TH-----LRGSLLESKCYIITVTPVPPGPGSPESMKAYLKQAAPSKGPTV-R 525
 QY 425 LQDAPPGTPAIAWGEVPRHQLRGLHLYTLCAQSGTSPSCVMNVSGTQSVTLPLDPLWGP 484
 DB 526 TKVKGNEAVLEWHDLPVDVQNGFIRNYSISYRTSVGKEMVVRVDSHTYETLSLSSDT 585
 QY 485 CELWVTAIAQGGPPGP---ILRLHLPDNTLRWKVLPGLPLWGLFLGCGLSLATSGR 541
 DB 586 LYMVMAAYTEGGKDGPEFTTLPKPAQGHIEALVVPVCL-----AFLTLTLLGVLF--- 638
 QY 542 CVHLRHKVLPVWVWKEKVPDPANSSGQ---PH-----MEQVPEAQPLGDLPILEVEE 590
 DB 639 CFNKR-DLIKKHWPVDPDSKSHIAQWSPHTPPRHFNFSKQDMQYSDANFTDVSVVVEIEA 697
 QY 591 MEPPP-----VMESSQP-----AQATAP--- 608
 DB 698 NNNKPCPDLDKSVDLFKKVKISTEGHSGIGSSCMSSSRPSISSSEENESAQSTASTVQ 757
 QY 609 ----LDSGYEKHFLLPT-----PEELGLL 627
 DB 758 YSTVHSGY-RHQVPSVQVFSRSESTQPLDSEERPEDLQLV 798

RESULT 9
 S17308
 leukemia inhibitory factor receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S17308
 R;Gearing, D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Price,
 EMBO J. 10, 2839-2848, 1991
 A;Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 signal t
 A;Reference number: S17308; MUID:92007727; PMID:1915266
 A;Accession: S17308
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1097 <GEA>
 A;Cross-references: UNIPROT:P42702; GB:X61615; NID:934365; PIDN:CAA43805.1; PID:934366
 Query Match 5.9%; Score 206.5; DB 2; Length 1097;
 Best Local Similarity 19.5%; Pred. No. 4.8e-06;

Matches 138; Conservative 108; Mismatches 269; Indels 193; Gaps 37;

QY 47 LGDLNCSWEP--LGDLCASSELHLQSQKYSRKNKTQTVAAGRSWVAIPRE----- 95
 Db 346 LKEIICSNPGRVTLVGP-----RATSYTLVESFGK-YVRLKRAEAPTNESYQ 394
 QY 96 ---QLTMSDKLLVWGTGKAGQPL---WPPVFVNLETOMKPNAPRLGPDVDFSDDDPLEAT- 148
 Db 395 LLEQMLPQEIYNTLNAHPLGRSOSTILVNIKEKYVHTP-----TSFKYKD-INSTA 448
 QY 149 --VHMAPPWPSPSHKVLICQFYHRCOEAAWTLLEPELKTPIPTPVE-----IODLELATGY 202
 Db 449 VKLSWHLPGNFAKINFLCEIIEIKNSV-----QEOBNVTIKGVENSYSVALDKLNEY 502
 QY 203 KVTG-----RCMEKEEDLWGEWS---PILSFQTPPSAPKDVWVSGNLCTGPGGEEPLLLWK 256
 Db 503 TLYTFTRICSTETFWK-WSKWNSKKQHLTTEATSPSKGPDWTRE-----WSSDGKNLIYWK 557
 QY 257 APGPCQVSKVWFVWVGRELSPEGITCCSLIPSGAEWAR-----VSAVNATS 305
 Db 558 -PLPINEANGKILSY--NVSCSDEETQSLEIPDPQHKAEIRLKDNDYIISVVAKNSVG 614
 QY 306 WEPLTNLSLVCLDSASAPR-SVAVSSIAGSTE-LLVTWQPGPELEHVVDWARD--GDP 361
 Db 615 SSPPSKIA-----SMEIPNDLLKIEQVGVGKGIILLTHYDPMNTCDYVVIKWCNSRSRSP 669
 QY 362 LEKLNWVRLPPGNLSALLPGN-FTVGVPPYRITVAVSAGSLASASSVWGFRELAPLVGP 420
 Db 670 C-LMDWRKVPNSNTEVIESDEFPRGIRYNFVLYGCRNOGYQLLRSIIGVYBELAPIVAP 728
 QY 421 TLWRLQDAPGTPAIAGVEPRHQLRGLHLYTL-----CAQSGTSPSCVN 467
 Db 729 N-FTVEDTSADSIILVWEDIPVEELRGFLGFLYFGKGERDTSKRVLESGRSLKVN 787
 QY 468 VSGNTQ-SVTLPDLPWGPC-ELWVTASTIAGQGP-----GPILRLHPDNTL 513
 Db 788 ITDISQKTLRIADLQKTSYHLVLRAYTDCGVGPEKSMVVTWKENSVGLIILAIIP--V 844
 QY 514 RWKVLPGILFLWGLFLGCGLSLATSGRCYHLRHKVLPWVME---KVPDPAN----- 563
 Db 845 AVAVIVGVW-----TSILCYRKR-----EWIKETFPDIPNENCKALOF 884
 QY 564 -----SSSGOPHMEQVPEAQPLGDLPILEVEEMEP-- 593
 Db 885 QKSVCEGSSALKTLEMNCTPNNVVELETSAPFKIEDTEIISPAERP-EDRSDAEPEN 943
 QY 594 -----PPVWESSQP-----AQATA-----PLDSGYEKHFLPTPEE 623
 Db 944 HVVVSYPPIIEEIPNPADEAGGTAQVIYIDVQSMYOPQAKPEBEQ 991

RESULT 10
 JX0312
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
 C:Accession: JX0312; JX2181; S38942
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
 J. Biochem. 115, 557-562, 1994
 A:Title: Three different cDNAs encoding mouse D-factor/LIF receptor.
 A:Reference number: JX0312; MUID:94334302; PMID:8056772
 A:Accession: JX0312
 A:Molecule type: mRNA
 A:Residues: 1-1092 <TOM>
 A:Cross-references: UNIPROT:P42703; DDBJ:D26177; NID:g473718; PIDN:BAA05165.1; PID:d1008
 A:Accession: JX2181
 A:Molecule type: mRNA
 A:Residues: 1-717, 'EA' <TOM>
 A:Cross-references: DDBJ:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494
 A:Experimental source: liver
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
 FEBS Lett. 334, 193-197, 1993
 A:Title: Pregnancy associated increase in mRNA for soluble D-factor/LIF receptor in mouse

A:Reference number: S38942; MUID:94039833; PMID:7901054
 A:Accession: S38942
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-717, 'EA' <TOM>
 A:Cross-references: GB:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494
 C:Keywords: differentiation; receptor; transmembrane protein
 F:1-43/Domain: signal sequence #status predicted <SIG>
 F:44-1092/Product: differentiating factor/leukemia inhibitory factor receptor
 F:828-854/Domain: transmembrane #status predicted <TM>

Query Match 5.9%; Score 206; DB 2; Length 1092;
 Best Local Similarity 20.3%; Pred. No. 5.1e-06;
 Matches 139; Conservative 93; Mismatches 256; Indels 198; Gaps 34;

QY 47 LGDLNCSWEP--LGDLCASSELHLQSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLL 104
 Db 341 LKEIICSNPGRITGLVGP-----RNTETLTFESISGKSAFHRIEGLTNETYRL 390
 QY 105 VMGTKAGQ-----PL---WPPVFVNLETOMKPNAPRLGPDVDFSDDDPLEATVH 150
 Db 391 GVQHPGGEIHNFLTGTGNPLGQAQSAVININTERVAPHDP---TSLKVKDINSTVVTFS 447
 QY 151 WAPPTWPSHKVLIQFYHRCOEAAWTLLEPELKTPIPTPVE-----IODLELATGY 203
 Db 448 WYLPNGFTKINLLCQIEICKANS-----KKEVRNATIRGAEDSTYHVAVDKLNPYATY 501
 QY 204 VYGRCEMEKEEDLWGEWS---ILSFQTPPSAPKDVWVSGNLCTGPGGEEPLLLWKAPGP 260
 Db 502 FRVRC-SKKTWFKWRSWDEKRLHTEATPSKGPDTWRE-----WSSDGKNLIIVWK-PLP 555
 QY 261 CVQVSKVWFVWVGRELSPEGITCCSLIPSGAEWARVSAVNATSWEPLTN----- 311
 Db 556 INEANGKILSY-----NVSCSL---NEETQSVLEI---FDPQHRAEIQLSKND 597
 QY 312 --LSLVCLDSASAPR-----VAVSSIAG-STEILLTWQPGPELEHVVDWA 356
 Db 598 YIISVVAARNASGSSPPSKIASMEIPNDITVEQAVGLGNRIFLTWHRDPNMTCDYVVIKWC 657
 QY 357 RD--GDPLEKNWVRLPPGNLSALLPGN-FTVGVPPYRITVAVSAGSLASASSVWGFREE 413
 Db 658 NSSREPC-LIDWRKVPNSNTEVIESQFQPGVRYNFYLYGCTNOGYQLLRSIIGVYEE 716
 QY 414 LAPLVGTLWRLQDAPGTPAIAGVEPRHQLRGLHLYTLCAQSGT----- 460
 Db 717 LAPIVAPN-FTVEDTSADSIILVWDDIPVEELRGFLGFLYFGKGERDTPKTRSLPEPH 775
 QY 461 SPSVCMNVSGNTQ-SVTLPDLPWGPC-ELWVTASTIAGQGP-----GPILRL 506
 Db 776 SDIKLKNITDISQKTLRIADLQKTSYHLVLRAYTHGGLGPEKSMFVVTWKENSVGLIITAI 835
 QY 507 HLPDNTLRWKVLPGLFLWGLFLGCGLSLATSGRCYHLRHKVLPWVME---KVPDPA 562
 Db 836 LIP---VAVAVIVGVW-----TSILCYRKR-----EWIKETFPDIPNPE 872
 QY 563 N-----SSSGOPHMEQVPEAQPLGDLPILEVEEMEP-- 588
 Db 873 NCKALQFQKSVCEGSSALKTLEMNCTPNNVVELESRSIVPKIEDTEIISPAERP-GER 931
 QY 589 EMEEP-----PPVWESSQP-----SQPA 603
 Db 932 SEVDPENHVVSYPPIIEEITNPA 957

RESULT 11
 A41527
 N:Alternative names: transforming protein axl; UFO receptor
 C:Species: Homo sapiens (man)
 C:Date: 28-May-1992 #sequence revision 05-Jan-1996 #text_change 09-Jul-2004
 C:Accession: A41527; B41527; E38269; I39203; G02782
 R:O'Bryan, J.P.; Frye, R.A.; Cogswell, P.C.; Neubauer, A.; Kitch, B.; Prokop, C.; Espinos
 Mol. Cell. Biol. 11, 5016-5031, 1991

[illegible]

QY 120 VNLETOMKENAPRLGPDVDFSEDDPLEATVHVAPPTWPSHKVL----- 162
Db 206 LKATSI-----LQWTEVPDPDHLRALRGTSLSQAQFWSSEG 243
QY 163 ICQFYHRCQEAWT-----LLEPELKT-----IPLTPVEIODLELATCYKYVGRCRME- 211
Db 244 ATSFHMLTDLGGTNTTAVIRQGVSTHTFLHLSQGTPELHKICASAGPHQIWGPSATEW 303
QY 212 -----KEEDLWGEW-----SPILSFQT-----P 229
Db 304 TYPSPSDDLPLRLNELWASKAGLGARDGYVLKLSGPMESTSTLGPBECNAVFPGLP 363
QY 230 P-----SAPKDVVWSGNLCGTPGGBEPLLLWKAPGPCQVQSYKWFVWGGRELS- 278
Db 364 PGHYTLQLKVLAGFYDAWVEGS---TWLAESAALPREVEFG-----ARLWLDGLEASK 412
QY 279 -----PEGIT---CCCSLIPSGAEWARVSNAVATSWEPLTNLSL 314
Db 413 QPGRALLYSDDAPGSLNISVPSGATHVIFCLVP-GAHY-RVDIASGTG---DISQSI 467
QY 315 VCLDSASAPRSVAVSSIAGSTELLVTPQPGGEPLLEHVVDWARDGDPLEKLNWRLPPGN 374
Db 468 SGYTSPLPQSLVSRSPSPLDIAWGPAPGLECYKVTWHDGSGRSPGDLVDLGPDT 527
QY 375 LS-----ALLPCNFTVGPRIITVAVS-ASGLASASSVWGFEELAPLVGPTLWRLQDA- 428
Db 528 LSLTLKSLVFGS-----SYTWSAWAWAGNLGSDSQKTHSCTRPA-----PTNLSLGFAH 577
QY 429 PPGTPAIAMEGEVPRHQLRGLHTHYLCAOSGTSVCMNVSGNTQSVTLPLDLPWGPCELM 488
Db 578 QPAALKASWHPGGRDAPHRLRYLRPLTLESEKV---LPREAQFNSWAQLTAG-CBEPQ 633
QY 489 VTASTI-----AGCGPGPILRLHLPDNT-----LRKWLP 520
Db 634 VQLSTLWGSRRSSANATGTPPSAPTLVNVTSDAPTQLQVSWAHVPG 681

RESULT 13
T46428
hypothetical protein DKFp434B2226.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46428
R:Ansoorge, W.; Winkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23028
A:Accession: T46428
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1185 <AAA>
A:Cross-references: UNIPROT:Q9NTD2; EMBL:AL137357
A:Experimental source: adult testis; clone DKFp434B2226
C:Genetics:
A:Note: DKFp434B2226.1

Query Match 4.7%; Score 164.5; DB 2; Length 1185;
Best Local Similarity 20.3%; Pred. No. 0.0036;
Matches 120; Conservative 68; Mismatches 194; Indels 209; Gaps 27;
QY 96 QLTWMSDKLLVWGTKA-----GQPLWPPVFVNLETQMK---FNAPRLGPDVDFSEDDPL 145
Db 231 QLTGLGKVLVEVQVLAFTRIQDGSFHPPI---LELTLDVFGPM---GILFPFVRIT 284
QY 146 EATVHVAPPTWPSHKVLICQFHYR-----RCQEAATWLLPELKIPLTPVEIODLEL----- 198
Db 285 SVRLIWQPPAAPNGIILAYQITHLRNTTANTATVEVLAPSQRYATGLKPSVYLFRI 344
QY 199 -ATGYKYVGRCR-----MEKEEDL-----W----- 217
Db 345 TAQTRKWGEAAEALVVTTEKRRDPQPSRPWQOEDVRARSVLLSWEPGSDGLSPVRY 404
QY 218 -----GEWS-----PILSFQTPPSAPKDVWS-----G 240

Db 405 TIQTRELPSGRWALHSASVSHNASSFIVDLRKPTSYKFRVKAATNDIGDSEFSSESBLT 464
QY 241 NLCOTPGGEBPLLI-----WKAPGPCVQVSYKWFVWGGRELSPEGIT---CC 285
Db 465 TLQAAP-DEAPTILSVTPHTTTSLVIRWQPPAEDKINGIILLGFRIRYRELLYEGRLGFTL 523
QY 286 CSLIPSGAEWA-----RVSANVATSWEPPLTNLS 313
Db 524 RGINNPGATWALTSMTSMRNLSPSLTYEOLDNLNKHRYEIRMSVYNVAVGEGSPSPQ 583
QY 314 LVCLDSA---SAPRSVAVSSIAGSTELLVTPQPGGEPL-----HVVDW-ARDGDPLE 363
Db 584 EVFVGEAVPTAAPRVVHVG-ATATQDVTWEPPLDSQNGDIQGYKIYFEWAQRGNLTE 642
QY 364 KLNWRLPPGNLSALLPCNFTVGPRIITVAVSASGLASASSVWGFEELAPLVGPTLW 423
Db 643 RVKTLFLAENSVKL---KNLTGYTAYMVSVAAFAAGDGPST-----PTQG 686
QY 424 RLQDAPPCTPA-----IAW-GEVPRHQLRGLHTHYLCAQ-SGTSPPSCMN 467
Db 687 QTOQAAPSAAPSVMKSELTTTSVNVSWEARQFPNGILLEGYRLVYPCSPVDGVSKIITVD 746
QY 468 VSGNT-----QSVT-----LPDLPWGPCELMVTAAGQPPGP 502
Db 747 VKGNSPLWLKVKDLAEGVTYFRIRAKTFTYGP-EIEANVTTPGEGAPGP 796

RESULT 14
T30581
neural cell adhesion molecule L1.1 - zebra fish (fragment)
C:Species: Brachydanio rerio (zebra fish)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30581
R:Tongiorgi, E.; Bernhardt, R.R.; Schachner, M.
J. Neurosci. Res. 42, 547-561, 1995
A:Title: Zebrafish neurons express two L1-related molecules during early axonogenesis.
A:Reference number: Z20875; MUID:96155762; PMID:8568941
A:Accession: T30581
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1197 <TON>
A:Cross-references: UNIPROT:Q90478; EMBL:X89204; NID:gl065713; PID:gl065714; PIDN:CAA614;
C:Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; in

Query Match 4.6%; Score 162.5; DB 2; Length 1197;
Best Local Similarity 22.0%; Pred. No. 0.005;
Matches 127; Conservative 80; Mismatches 212; Indels 159; Gaps 34;
QY 26 LFORTRPQGSAGPLQCYGVG-PLGDLNCSWEPLDGLGAPSELHLQSQKYRSNKTKQTVAVA 84
Db 370 LYQAT--AGQTVMLDCRTFGSPLPKIH--WEILDSIPALSNAKISQTTNGSLKISNVSEE 425
QY 85 AGRSWAIPRE--QLTMSDKLLVWGTKAGQDLWPPVFVNLETQMKPNAPRLGPDV----D 138
Db 426 DSNRYTCSVSETNKSISADVEVLNRTKI---VGPP--QNLHVIR-----GSDAILHCK 473
QY 139 FSEDDPLEA-TVHMAPPTWPSHKVLIC---QFHYRRCQEAATWLLPELKIPLTPVEI 193
Db 474 YTVDNHLSKSPVQW---NKDGHKITASTSNKYHE---IEGSLKVLVDQMEDMGSIYCEV 527
QY 194 Q---DLELATGYKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVVWSGNLCGTPGSEE 250
Db 528 STTLSDSTASGY-----ITVQDKPDPQSLKLSKX-----BRS 561
QY 251 PULLWKAQPCVQVSYKWFVWGGRELSPEGITCCCSLIPSGAEWARVSAV--NATSWEP 308
Db 562 VTISWM---PSYENNSPVTEYV--IEMN-EGET-----PDEGQMKYRSVSQDIDSWRS 609
QY 309 LTNLS-----LVCLDSASAPRSVAVSSIAGST-----ELLVTW 341
Db 610 ICSYKYHFQIRAVNSIGTSAPTE---SLSYSTPAKPDTPNPENVMVTLSTDPKSMIISW 666

Qy 342 QP-----GRCEPLEHVVDWARDDPLEKLNW-----VRLPPGNLSALLPQNFVGVDPYR 390
Db 667 QEMDRROFNGFG--FOYKVFRRRAAD--SGAHWTSESSVSNPP-----LMVNNTGTFVSFE 717
Qy 391 ITVTAVSASGLA-SASSVMGPRELAPLVGPTLWRLQDAPGTPAIANGVEVPRHQLRGHL 449
Db 718 IKVQAVNDLGAPEPLTVIGSGDFPLEAPSAUSVTELOKTSVMWRVSPVRPESVRGHL 777
Qy 450 THYTLCAQSPTS-----PSVCMNVSGNTQSVTLP-----DLP-WGPCELMWTASTIA 495
Db 778 LGYKIVLRMGKSQWETPGRAVSSSGNPTVIEVPADAAEKIVSDLOFYSDYDITLITAFNSK 837
Qy 496 GQGP-----PGPIRLHL-----PDNTRLWK 516
Db 838 GEGPHSESTPEGAPGVLFPLFPDSPSESEITLRWE 875

RESULT 15
C88400
protein H19W22.1 [imported].. Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C88400
P:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:9069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: C88400
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1825 <STO>
A:Cross-references: UNIPROT:Q9UB28; UNIPROT:Q9UB29; GB:chr_III; PIDN:AAB94997.1; PID:g27
C:Genetics:
A:Gene: H19W22.1
A:Map position: 3

Query Match 4.5%; Score 159; DB 2; Length 1825;
Best Local Similarity 21.2%; Pred. No. 0.015;
Matches 128; Conservative 76; Mismatches 245; Indels 156; Gaps 32;

Qy 105 VMGTYK-----AGQPLMPPVFNLETKMKNAPR-LGPDVDFSDDDPLEATVHWAPPTWP 157
Db 1 MWSVKIRAINSAHSATPA---AQTKTPGGELIIGFDVSYRQKPI---ISWRSKENT 54
Qy 158 SHKVLICQFYHRCQEAATLLEPELTIPLT-----PVEIQDLELATGYKVGRCRMEKE 213
Db 55 NDLESFVLEWKSTESSW---RQHRNPIFYNGWQRFPYSVDLGGELPQGHYQVRI-VAKD 110
Qy 214 EDLMGEW-SPLISFOT-----PPSAPKDVWVSGNLGCTPGGEPDLLWKAPGPC-VOVS 265
Db 111 PNRGNATSPVQVQVOTOSQKAPRAPADVQVS-----PL-----GPTQIRVQ 153
Qy 266 Y-----KVMFWGRELSPGEGITCCCSLIPSGAEWARVSAVNATSWEPFLTNLSL 314
Db 154 WAPLHESEWNCRLWYIVKHSITPQNGF---KNLTNGENFVVDSDPYTQW---NFEV 205
Qy 315 VLDSAS-----APRSVAVSSI---AGSTELLVWQPGGEPLEHVVDWAR 357
Db 206 QAANPAGESOWSRAQSQTQGVAFGAVANLRVQIPGDSLQCSNQW-PVNPNGRITQY-- 262
Qy 358 DGDPLEKLVRLPPGNL--SALLPGNFTVGPV-----YRITVTAVSASGLAS 403
Db 263 -----EVTYQLISRGCDNNOEAPRTITVNGPHFTTGLPHSKYRVGVAASNAGGE 316
Qy 404 ASSVMGPRELAPLVGPTLWRLQDAPGTPAIANGVEVPRHQLRGHLTHYTLCAQSG--- 459
Db 317 RVSLIEIQDQAAPSGAPLYLRTEDIRFTDVSISWQAPPCQTNGEITEYEYEVTAGDRRQ 376
Qy 460 TSPSVCMNVSG-----NTQSVTLDDL-----WGPCELMWTASTIAGO---GPPGP 502
Db 377 TVQKTTENIRGTRAKIENLOPQTRYNVKVRAYTARGAGPWSDEVFPQTSAGQQNVQAPGF 436

Qy 503 ILRLHL-PDNT-LRWK---VLPGLFLWGLFLGCGLSLATSRCYHLRHKVLPRLRWWEK 557
Db 437 VKVLHTGADNAQLVWQSPYENPGVV-----DKYKCRYAPSGTQOYQE 478
Qy 558 VPDPAANSSSQPHMEQ--VPEAQPLGDLPLILEVEEMEPVPPVMESSQPAQATAPL-DSGYE 614
Db 479 RQFPFVAVSPCCOQRIERQNLPSPPGSRHLHCGRIENLRP-----EQTYDFQVSAHVKDSGWG 534
Qy 615 KHFLP 619
Db 535 PYSPP 539

Search completed: February 19, 2005, 01:16:51
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 19, 2005, 01:06:05 ; Search time 181 Seconds
(without alignments)
1799.350 Million cell updates/sec

Title: US-10-088-950A-1

Perfect score: 3498

Sequence: 1 MRGGRGAPFWLPLPKALL.....FLTPBELGLGPPRPQVLA 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	2 O60624	O60624 homo sapien
2	3494	99.9	636	2 O6UWB1	O6UWB1 homo sapien
3	2044	58.4	623	2 O70394	O70394 mus musculus
4	380	10.9	862	1 I12S_HUMAN	O99665 homo sapien
5	329	9.4	861	1 I12S_PIG	O8mj51 sus scrofa
6	328.5	9.4	874	1 I12S_MOUSE	F97378 mus musculus
7	326.5	9.3	861	1 I12S_BOVIN	O9beg2 bos taurus
8	313	8.9	870	2 O6UANO	O6uan0 tetraodon n
9	297.5	8.5	836	1 GCSR_HUMAN	O99062 homo sapien
10	296	8.5	962	2 O65214	O65214 rattus norv
11	292	8.3	971	2 O70458	O70458 mus musculus
12	288.5	8.2	970	2 O88821	O88821 mus musculus
13	277	7.9	837	1 GCSR_MOUSE	P40223 mus musculus
14	250	7.1	918	1 I12S_HUMAN	P40189 homo sapien
15	248	7.1	917	1 I12S_MOUSE	O00560 mus musculus
16	248	7.1	917	2 O6PDI9	O6pdi9 mus musculus
17	244	7.0	813	2 O6DD37	O6dd37 xenopus lae
18	243.5	7.0	813	2 O6UANI	O6uan1 tetraodon n
19	241.5	6.9	918	2 O9WCU9	O9wcu9 gallus gall
20	237.5	6.8	881	2 O57519	O57519 xenopus lae
21	229	6.5	710	2 O57520	O57520 xenopus lae
22	226.5	6.5	918	1 I12S_RAT	P40190 rattus norv
23	226	6.5	979	2 O99650	O99650 homo sapien
24	216	6.2	1010	2 O7TQ89	O7tq89 rattus norv
25	212.5	6.1	1083	2 O8QFQ7	O8qfq7 gallus gall
26	212	6.1	1093	2 O70535	O70535 rattus norv
27	207	5.9	649	2 O6EBC6	O6ebc6 homo sapien
28	207	5.9	662	2 O6EBC3	O6ebc3 homo sapien
29	207	5.9	732	2 O8N117	O8n117 homo sapien
30	207	5.9	764	2 O6EBC4	O6ebc4 homo sapien
31	206.5	5.9	1097	1 LIFR_HUMAN	P42702 homo sapien

32	206	5.9	1092	1 LIFR_MOUSE	P42703 mus musculus
33	193	5.5	582	2 O6UWL8	O6uwl8 homo sapien
34	191	5.5	1304	1 NRCA_HUMAN	O92823 homo sapien
35	185	5.3	844	2 O6UAM8	O6uam8 tetraodon n
36	184.5	5.3	894	2 O6UAM7	O6uam7 tetraodon n
37	182	5.2	716	2 O8RS01	O8rs01 mus musculus
38	181	5.2	716	2 O8K5B1	O8k5b1 mus musculus
39	178.5	5.1	662	2 O6EAL7	O6eal7 mus musculus
40	178	5.1	894	2 O8NSL2	O8nsl2 homo sapien
41	174.5	5.0	509	2 O8WYJ0	O8wyj0 homo sapien
42	174	5.0	686	2 O6UAM9	O6uam9 tetraodon n
43	173.5	5.0	1284	2 F91767	F91767 manduca sex
44	171	4.9	1933	2 O6V3A4	O6v3a4 mus musculus
45	170.5	4.9	547	2 O6EAL6	O6eal6 mus musculus

ALIGNMENTS

RESULT 1

O60624 PRELIMINARY; PRT; 636 AA.

AC O60624; (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Class I cytokine receptor (CRL1 protein).
GN Name=WSX1; Synonyms=CRL1, IL27RA;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98262921; PubMed=9600072; DOI=10.1006/bbrc.1998.8576;

RA Sprecher C.A., Grant P.J., Baumgartner J.W., Fresnel S.R.,

RA Schrader S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;

RT "Cloning and characterization of a novel class I cytokine receptor.";

RL Biochem. Biophys. Res. Commun. 246:82-90 (1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Zhang W., Wan T., He L., Yuan Z., Cao X.;

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF053004; AAC39755.1; -.

submitted
in IDS

OS	Homo sapiens (Human).	Query Match	99.98;	Score 3494;	DB 2;	Length 636;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Best Local Similarity	99.98;	Pred. No. 5.3e-223;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Matches 635;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
NCBI	TaxID=9606;					
OX	[1]					
RN	SEQUENCE FROM N.A.					
RP	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,					
RA	Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,					
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,					
RA	Godowski P.;					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment."					
RL	Genome Res. 13:2265-2270(2003).					
DR	EMBL; AY358876; AA089235.1; -.					
DR	InterPro; IPR003961; FN.III.					
DR	InterPro; IPR008957; FN.III-like.					
DR	Pfam; PF00041; fn3; 2.					
DR	SMART; SM00060; FN3; 3.					
DR	PROSITE; PS50853; FN3; 2.					
SQ	SEQUENCE 636 AA; 69459 MW; 473BAAAABD0502B9 CRC64;					
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DB	1 MRGGGFPWLWPLPKLALLPWLVLVLFQTRPGSAGPLQCYGVGGLDNCSEWPLGDL 60					
QY	61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPWPVFV 120					
DB	61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPWPVFV 120					
QY	121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQPHYRRCQEAATLLE 180					
DB	121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQPHYRRCQEAATLLE 180					
QY	181 PELKTIPLTPVEIQDELATQYKVGCRMEKEDLWGEWSPILSQTTPSPAPKDVWSG 240					
DB	181 PELKTIPLTPVEIQDELATQYKVGCRMEKEDLWGEWSPILSQTTPSPAPKDVWSG 240					
QY	241 NLCGTPGGEELPILWKAPGPCVQVSYKVMWVGRELSPGEGITCCCSLIPSGAEWARVSA 300					
DB	241 NLCGTPGGEELPILWKAPGPCVQVSYKVMWVGRELSPGEGITCCCSLIPSGAEWARVSA 300					
QY	301 VNATSWEPITNLISLVCLDSASAPRSVASSIAGSTELLTWQPGGPELHVVDWARDGD 360					
DB	301 VNATSWEPITNLISLVCLDSASAPRSVASSIAGSTELLTWQPGGPELHVVDWARDGD 360					
QY	361 PLEKNWRLPPGNLSALLPGNFTVGPYRITVTVASGLASSVWGFRFELAPLVGP 420					
DB	361 PLEKNWRLPPGNLSALLPGNFTVGPYRITVTVASGLASSVWGFRFELAPLVGP 420					
QY	421 TLWRLQADPPGTPALWGEVPRHQLRGHLTHYTLCAQSGTSPVCNMVNSGNTQSVTLPLD 480					
DB	421 TLWRLQADPPGTPALWGEVPRHQLRGHLTHYTLCAQSGTSPVCNMVNSGNTQSVTLPLD 480					
QY	481 PWGPCELWVTASTIAGQGGPPIRLHLDPNTLWKLPGILFLWGLFLGCGLSIATSG 540					
DB	481 PWGPCELWVTASTIAGQGGPPIRLHLDPNTLWKLPGILFLWGLFLGCGLSIATSG 540					
QY	541 RCYHLRHKVLPWWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEWEMPPPWESS 600					
DB	541 RCYHLRHKVLPWWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEWEMPPPWESS 600					
QY	601 QPAQATAPLDSGYEKFHTPEELGLLGP RPQVLA 636					


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DB 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
|||||
RESULT 3
O70394
ID 070394 PRELIMINARY; PRT; 623 AA.
AC O70394
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Class I cytokine receptor (Interleukin 27 receptor, alpha).
GN Name=il27ra; Synonyms=Wsx1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98262921; PubMed=9600072; DOI=10.1006/bbrc.1998.8576;
RA Sprecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,
RA Schrader S.K., Yamaguchi T., Whitmore T.E., O'Hara P.J., Foster D.F.;
RT "Cloning and characterization of a novel class I cytokine receptor.";
RL Biochem. Biophys. Res. Commun. 246:82-90(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF053005; AAC40121.1; -
DR ENBL; BC032878; AAH32878.1; -
DR HSSP; P05710; 1P6F.
DR MGD; MGI:1355318; Il27ra.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0042607; F:exogenous peptide antigen binding; IDA.
DR GO; GO:0045509; F:interleukin-27 receptor activity; IDA.
DR GO; GO:0042287; F:MHC protein binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR003961; FN III.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS00853; FN3; 2.
KW RECEPTOR.
SQ SEQUENCE 623 AA; 68998 MW; 4BA20FEC875A7180 CRC64;

Query Match 58.4%; Score 2044; DB 2; Length 623;
Best Local Similarity 62.8%; Pred. No. 5.2e-127;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;
```

```
QY 14 LPKALLPLLVLFQRTTRPGQSAGPLQCYGVGPGDLNCSWEPGLDGAPSEHLQSQKY 73
DB |||||
DB 9 LTPLELLLSLMSLLGTRPHGSPGLQCYSGVPLGILNCSWEPGLDLETPPVLYHQSKY 68
|||
QY 74 RSNKTQTVAAAGRSWAIPREQLTMSDKLLVNGTKAGQPLWPPVFNLTQMKPNAPRL 133
DB |||||
DB 69 HPNRVMEVKPSKOSWVTIPREQFTWADKLLIWTQKGRFLMSVSVNLETQMKPDTPQI 128
|||
QY 134 GPQVDFSEDDPLEATVHWAPPTWPSHKVLICQHYRRQCAAAWTLLEPELTKTPTLTPVEI 193
DB |||||
DB 129 FSQVDISEATLEATVQWAPPPVPPQKALTQCFRYKECAEATRLPEPQKTDGLTPVEM 188
|||
QY 194 QDLELATGYKYGRCRMEKEEDLWGSWSPILSQTTPPSAPKVVVSGNLGCTPGGEPLL 253
DB |||||
DB 189 QNLEPGTCYQSGRCQVENGYP-WGEWSSPLSFOTPFDPEDVWVSGTVCETSGKRAALL 247
|||
QY 254 LMKAPGCVQVSYKVMFWVGGRELSPGEGITCCSLIPSGAEWARVSAVNATSWPLTNLS 313
DB |||||
DB 248 VKMDPRPCQVTVTVWFGAGDITTTQEEVPCCKSPVPMWENAVVSGNSTSWVPPTNLS 307
|||
QY 314 LVCLDSASAPRSVAVSGSIAGSTELLVTWQPGCEPLEHVVDWARDGDPLEKLNWVRLPPG 373
DB |||||
DB 308 LVCLAPESAPCDVGSADSGPGIKVTKQGTREKPLEYVVDWAQDGDSDLKLNWTRLPFG 367
|||
QY 374 NLSALLPGNFTVGVYRITVTAVSAGLASASSVWGFREELAPLVGPTLWRLQDAPPGTP 433
DB |||||
DB 368 NLSTLLPGEGKGVYRITVTAVYSGLAAPSAVWGFREELVPLAGVAVWRLPDDPPGTP 427
|||
QY 434 AIANGVPRHOLRGHLTHYTLCAQSGTSVSVCMVSGNTQSVTLDPWGPCELWVWTAST 493
DB |||||
DB 428 VWANGVPRHQLRGQATHYTFICQSRGLSTVCRVSSQTQTATLPNLHSGSFKLWTVST 487
|||
QY 494 IACQGGPGPTILRLHLPDNTLRWKLPGILFLWGLLGLGCLSLATS----GRCVHLRHKV 549
DB |||||
DB 488 VACQGGPGDLSUHLPDNRIRWKLWFLSLWGLLGLGCLSLATSCTCQARCLWHRKL 547
|||
QY 550 LPRWVWEKVPDPANSSGGPHMBOVPEAQPLGLDPLILEVEEMPPPPVMESSQPAATAPL 609
DB |||||
DB 548 LPQWIERVDPDPANSSGGPYIKEVSLPQPKDGPILVEVEELQPVVES--PKASAPI 604
|||
QY 610 DSGYEGHFLPTPEELGILL 627
DB |||||
DB 605 YSGYEGHFLPTPEELGILL 622
|||
```

RESULT 4

```
ID 112S_HUMAN STANDARD; PRT; 862 AA.
AC Q99665;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2)
DE (IL-12R-beta2).
GN Name=IL12RB2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; PubMed=8943050; DOI=10.1073/pnas.93.24.14002;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT "A functional interleukin 12 receptor complex is composed of two beta-
RL type cytokine receptor subunits.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=T-cell;
RX PubMed=10663559;
RA van Rietschoten J.G.I., Smits H.H., Westland R., Verweij C.L.,
```

RA den Hartog M.T., Wierenga E.A.;
 RT "Genomic organization of the human interleukin-12 receptor beta2-chain
 RT gene."; [3]
 RL Immunogenetics 51:30-36(2000).
 RN
 RP INTERACTION WITH STAT4, AND MUTAGENESIS OF LEU-801; PRO-802; SER-803
 RP AND ASN-804.
 RX PubMed=10415122; DOI=10.1006/abbi.1999.1302;
 RA Yao B.B., Niu P., Surowy C.S., Paltynek C.R.;
 RT "Direct interaction of STAT4 with the IL-12 receptor."; [4]
 RL Arch. Biochem. Biophys. 368:147-155(1999).
 RN
 RP INTERACTION WITH JAK2, AND MUTAGENESIS OF TYR-678; TYR-767 AND
 RP TYR-800.
 RX PubMed=10198225; DOI=10.1006/bbrc.1999.0479;
 RA Yamamoto K., Shibata F., Miura O., Kamiyama R., Hirose S.,
 RA Miyasaka N.;
 RT "Physical interaction between interleukin-12 receptor beta 2 subunit
 RT and Jak2 tyrosine kinase: Jak2 associates with cytoplasmic membrane-
 RT proximal region of interleukin-12 receptor beta 2 via amino-
 RT terminus."; [5]
 RL Biochem. Biophys. Res. Commun. 257:400-404(1999).
 RN
 RP INTERACTION WITH STAT4, AND MUTAGENESIS OF TYR-678; TYR-767 AND
 RP TYR-800.
 RX PubMed=9890938; DOI=10.1074/jbc.274.4.1875;
 RA Naeger L.K., McKinney J., Salvekar A., Hoey T.;
 RT "Identification of a STAT4 binding site in the interleukin-12 receptor
 RT required for signaling."; [6]
 RL J. Biol. Chem. 274:1875-1878(1999).
 RN
 RP TISSUE SPECIFICITY, AND INDUCTION.
 RX PubMed=9120388;
 RA Rogge L., Barberis-Maino L., Biffi M., Passini N., Presky D.H.,
 RA Gubler U., Sinigaglia F.;
 RT "Selective expression of an interleukin-12 receptor component by human
 RT T helper 1 cells."; [7]
 RL J. Exp. Med. 185:825-831(1997).
 RN
 RP PHOSPHORYLATION, INTERACTION WITH SOCS3, AND MUTAGENESIS OF TYR-678;
 RP TYR-767 AND TYR-800.
 RX PubMed=14559241; DOI=10.1016/j.bbrc.2003.09.140;
 RA Yamamoto K., Yamaguchi M., Miyasaka N., Miura O.;
 RT "SOCS-3 inhibits IL-12-induced STAT4 activation by binding through its
 RT SH2 domain to the STAT4 docking site in the IL-12 receptor beta2
 RT subunit."; [8]
 RL Biochem. Biophys. Res. Commun. 310:1188-1193(2003).
 RN
 RP VARIANTS GLY-313 AND ARG-720.
 RX PubMed=10600539; DOI=10.1006/bbrc.1999.1859;
 RA Matsui E., Kaneko H., Fukao T., Teramoto T., Inoue R., Watanabe M.,
 RA Kasahara K., Kondo N.;
 RT "Mutations of the IL-12 receptor beta2 chain gene in atopic
 RT subjects."; [9]
 RL Biochem. Biophys. Res. Commun. 266:551-555(1999).
 CC
 CC -1- FUNCTION: Receptor for IL-12. This subunit is the signaling
 CC component coupling to the JAK2/STAT4 pathway. Promotes the
 CC proliferation of T-cells as well as NK cells. Induces the
 CC promotion of T-cells towards the Th1 phenotype by strongly
 CC enhancing IFN-gamma production.
 CC
 CC -1- SUBUNIT: Heterodimer/heterotrimer; disulfide-linked. The
 CC functional high affinity IL12 receptor is composed of IL12RB1 and
 CC IL12RB2. IL12RB2 binds JAK2 (via its N-terminal) through a
 CC membrane-proximal region of the cytoplasmic domain. Interaction,
 CC in vitro and in vivo, with SOCS3 (via its SH2 domain) inhibits the
 CC STAT4-mediated activation. Binds STAT4 through a membrane-distal
 CC C-terminal region.
 CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q99665-1; Sequence=Displayed;
 CC Name=2;

CC IsoId=Q99665-2; Sequence=VSP_011112, VSP_011113;
 CC TISSUE SPECIFICITY: Isoform 2 is expressed at similar levels in
 CC both naive and activated T-cells.
 CC -1- DEVELOPMENTAL STAGE: Maximum levels in Th1 cells between day 3 and
 CC day 8 of activation.
 CC
 CC -1- INDUCTION: In vitro, up-regulated by interferon alpha.
 CC
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC
 CC -1- PTM: On IL12 binding, phosphorylated on C-terminal tyrosine
 CC residues by JAK2. Phosphorylation on Tyr-800 is required for STAT4
 CC binding and activation, and for SOCS3 binding.
 CC
 CC -1- POLYMORPHISM: Heterozygotic variants Gly-313 and Arg-720 are
 CC associated with atopy, an immunological condition that can lead to
 CC clinical symptoms such as allergic rhinitis, sinusitis, asthma and
 CC eczema.
 CC
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC
 CC -1- SUBFAMILY: Contains 5 fibronectin type III domains.
 CC
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
 CC
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 CC
 CC EMBL; U64198; AAB36675.1; -;
 CC HSSP; P05710; 1P6F.
 CC Genew; HGNC:5972; IL12RB2.
 CC MW; 601642; C: integral to plasma membrane; TAS.
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004907; F: interleukin receptor activity; TAS.
 CC GO; GO:0007166; P: cell surface receptor linked signal transdu. ; TAS.
 CC GO; GO:0008284; P: positive regulation of cell proliferation; TAS.
 CC InterPro; IPR002996; Cytokn recept_B/G.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR003529; Hemtrecept_1302.
 CC InterPro; IPR010457; Lep_receptor_19.
 CC Pfam; PF00041; fn3; 3.
 CC Pfam; PF06328; Lep_receptor_Ig; 1.
 CC PROSITE; PS50853; FN3; 5.
 CC PROSITE; PS01353; HEMATOPO REC L_F2; 1.
 CC Alternative splicing; Glycoprotein; Phosphorylation; Polymorphism;
 CC Receptor; Repeat; Signal; Transmembrane.
 CC SIGNAL 1 23 Potential.
 CC CHAIN 24 862 Interleukin-12 receptor beta-2 chain.
 CC DOMAIN 24 622 Extracellular (potential).
 CC TRANSMEM 623 643 Potential.
 CC DOMAIN 644 862 Cytoplasmic (potential).
 CC DOMAIN 154 218 Fibronectin type-III 1.
 CC DOMAIN 254 316 Fibronectin type-III 2.
 CC DOMAIN 317 415 Fibronectin type-III 3.
 CC DOMAIN 420 517 Fibronectin type-III 4.
 CC DOMAIN 521 617 Fibronectin type-III 5.
 CC DOMAIN 208 211 Poly-Ser.
 CC DOMAIN 750 753 Poly-Pro.
 CC SITE 305 309 WSXWS motif.
 CC SITE 662 670 Box 1 motif.
 CC SITE 796 801 Required for STAT4 binding.
 CC MOD_RES 800 800 Phosphotyrosine.
 CC CARBOHYD 48 129 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 129 129 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 166 166 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 195 195 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 271 271 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 347 347 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 376 376 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 480 480 N-linked (GlcNAc...) (potential).

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FT VARSPLIC 650 659 VFVLLAALRP -> RHSCPWTGS (in isoform 2).
FT VARSPLIC 660 862 Missing (in isoform 2).
FT VARSPLIC 660 862 /FTid=VSP_011112.
FT VARSPLIC 660 862 /FTid=VSP_011113.
FT VARSPLIC 660 862 I -> V (in dbSNP:2307146).
FT VARSPLIC 660 862 /FTid=VAR_014805.
FT VARSPLIC 660 862 T -> I (in dbSNP:7526769).
FT VARSPLIC 660 862 /FTid=VAR_019525.
FT VARSPLIC 660 862 R -> G.
FT VARSPLIC 660 862 /FTid=VAR_019526.
FT VARSPLIC 660 862 G -> R (in dbSNP:2307148).
FT VARSPLIC 660 862 /FTid=VAR_014806.
FT VARSPLIC 660 862 Q -> H (in dbSNP:2307145).
FT VARSPLIC 660 862 /FTid=VAR_014807.
FT VARSPLIC 660 862 G -> D (in dbSNP:2307153).
FT VARSPLIC 660 862 /FTid=VAR_014808.
FT VARSPLIC 660 862 A -> V (in dbSNP:2307154).
FT VARSPLIC 660 862 /FTid=VAR_016097.
FT VARSPLIC 660 862 H -> R.
FT VARSPLIC 660 862 /FTid=VAR_019527.
FT MUTAGEN 678 678 Y->F: No loss of STAT4 activation. No
FT MUTAGEN 678 678 loss of SOCS3 binding.
FT MUTAGEN 678 678 Y->R: No loss of STAT4 activation. No
FT MUTAGEN 678 678 loss of SOCS3 binding.
FT MUTAGEN 678 678 Y->E: Loss of STAT4 activation. Abolishes
FT MUTAGEN 678 678 SOCS3 binding.
FT MUTAGEN 678 678 L->A: Abolishes in vitro STAT4 binding to
FT MUTAGEN 678 678 a phosphorylated Y-800 peptide.
FT MUTAGEN 678 678 P->A: No effect on in vitro STAT4 binding
FT MUTAGEN 678 678
Query Match 10.9%; Score 380; DB 1; Length 862;
Best Local Similarity 25.3%; Pred. No. 1.1e-16;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;
FT 31 RPOGSAFLQCYGVPLGDLNCSWEPLGD-----LGAPSELHLSQ----- 71
DB 126 QPQN-----LSCIQKEGQGVACTWGERDTHLYTEYTLQSGPKNLTWQCKDIYCDYL 181
QY 72 -----KYRSMKTTQV-AVAGRSWAIPAIREQLTMSDKLAWGTGKAGQPLMPPVFN 121
DB 182 DFGINLTPESPESNFTAKVTAVNSLGSSSSLP-STFTFLDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNARLPGDVFSDDEPLEATVHWAPPTWPSHKVLIQCFHYRRCOEAAWTLLEP 181
DB 232 IKFO-KASVSR-----CTLYWR-----DEGLVLLNRLRYRPSNRLWN-- 269
QY 182 ELKTIPLTPV-----EIODLELATCYKYVGRCMKEEDLWGESPILSFOTP---PSAPX 234
DB 270 -----VNVTKAKGRHDLDLKPFTEYEFQISKLHLXKGSWSDWSESRLAQTPEEPTGML 325
QY 235 DVWVSGNLCTPGGEERPLLWK-----APGCVQVSRYKWFVWVGRELSPG--GITCCC 286
DB 326 DVWYMKRHIDY-SRQQLSLFWKLSVSEARGKILHYQVTLQELTGKAMQNTIGHTSWT 384
QY 287 SLIPSGAEWA-RVSAVNA--TSWEPLNLNLSVLCDSASAPRSVAVSSIAGSTELLVTWQP 343
DB 385 TVIPRTGNWAVAVSAANSKGSLSPLTRINIMNCEAGLLAPROVSANS-EGMDNLTWQP 443
QY 344 ---GPGEPLHVDWAR---DGDPLEKLNVRPLPGNLSALLPGNFTVGVPIYITVAVS 397
DB 444 PRKDPASQVQVYVWEWRELHPGGDTQVPLNLRSPYNVSAISGENTKSYICYRIVYALS 503
QY 398 ASGLASASSVWGFEELAPLVGPTLWRLQDAPCTPAIANGVPRHQLRGLHLYTLC-- 455
DB 504 GD-QGGCSSILGSKXKAPLSGPHNAITE-BKGSILISWNSIPVQMGCLLHYRIYWK 561
QY 456 -AQSGTSPSVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGQGPFGPIRLHLDPN 511
DB 562 ERDSNSQQLCEIPYRVSONSHPIINSLQ-PRVTVLLMWTALTAAAGSSHGNEREFCL-QG 619
QY 512 TLRWK--VLPGI---LFLWGLFLLCGGLSLATSGRCVHLRHKL------PRWWEKVP 559
DB 620 KANWMAFVAPSICIAIIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667
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QY 560 DPANSSSGQPH-----MEQVPEAQPLGDLFILEVEEMEPVPPVNMESSQAQATA-----PLD 610
DB 668 DPANSTCAKKYPTAEKTKQLPLDLRLLDWTPB---DPEPLVISEVLHVQVTPVFRHPPC 723
QY 611 SGYEKHLFPLPELGLLG-----PPRQVL 635
DB 724 SNWPQ-----REKGIQGHQASEKMMHSSASSPPPRAL 756

RESULT 5
IL2S_PIG STANDARD; PRT; 861 AA.
AC Q8MJ51; Q8WN24;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 beta2 receptor)
DE (IL-12beta2).
GN Name=IL12RB2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=peripheral blood monocytes;
RX PubMed=12543551; DOI=10.1016/S0165-2427(02)00288-X;
RA Kokubo T., Inumaru S., Watanabe S., Kubota T.;
RT "Cloning of porcine interleukin (IL)-12 receptor beta2 (IL-12beta2)
RT gene and its application to a rapid biological assay for human/porcine
RT IL-12.";
RL Vet. Immunol. Immunopathol. 91:155-160(2003).
RN [2]
SEQUENCE OF 12-859 FROM N.A.
RP TISSUE=Lymphoblast;
RX PubMed=12383645; DOI=10.1016/S0165-2427(02)00205-2;
RA Solano-Aguilar G.I., Zarlenga D., Beshah E., Vengroski K.,
RA Gasbarre L., Junker D.E., Cochran M.D., Weston C.O., Valencia D.M.,
RA Chiang C., Dawson H.D., Urban J.F. Jr., Lunney J.K.;
RT "Limited effect of recombinant porcine interleukin-12 on porcine
RT lymphocytes due to a low level of IL-12 beta2 receptor.";
RL Vet. Immunol. Immunopathol. 89:133-148(2002).
RN [3]
ERRATUM.
RA Solano-Aguilar G.I., Zarlenga D., Beshah E., Vengroski K.,
RA Gasbarre L., Junker D.E., Cochran M.D., Weston C.O., Valencia D.M.,
RA Chiang C., Dawson H.D., Urban J.F. Jr., Lunney J.K.;
RL Vet. Immunol. Immunopathol. 95:183-183(2003).
CC -I- FUNCTION: Receptor for IL-12. This subunit is the signaling
CC component coupling to the JAK2/STAT4 pathway.
CC -I- SUBUNIT: Heterodimer/heterotrimer; disulfide-linked. The
CC functional high affinity IL12 receptor is composed of IL12RB1 and
CC IL12RB2. IL12RB2 binds JAK2 (via its N-terminal) through a
CC membrane-proximal region of the cytoplasmic domain (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -I- PTM: On IL12 stimulation, phosphorylated on C-terminal tyrosine
CC residues (By similarity).
CC -I- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 2.
CC -I- SIMILARITY: Contains 5 fibronectin type III domains.
CC
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CC promotion of T-cells towards the Th1 phenotype by strongly
 CC enhancing IFN-gamma production. Can also activate STAT3.
 CC -!- SUBUNIT: Heterodimer/heterotrimer; disulfide-linked. The
 CC functional high affinity IL12 receptor is composed of IL12RB1 and
 CC IL12RB2. IL12RB2 binds JAK2 (via its N-terminal) through a
 CC membrane-proximal region of the cytoplasmic domain (5b
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in developing T helper (TH) cells.
 CC -!- DEVELOPMENTAL STAGE: Expressed at high levels in Th1 cells on day
 CC 3, 5 and 7 after primary activation. Very low expression in Th2
 CC cells on day 3 and not detectable on day 5 nor day 7 after
 CC activation.
 CC -!- INDUCTION: Following T cell activation, expression inhibited by
 CC IL4 and induced by IFN gamma.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -!- PTM: On IL12 stimulation, phosphorylated on C-terminal tyrosine
 CC residues. Phosphorylation of any one of Tyr-757, Tyr-804 or Tyr-
 CC 811 can activate STAT4, IFN-gamma production, and T-cell
 CC proliferation. Tyr-811 is the dominant site of cell proliferation.
 CC -!- MISCELLANEOUS: Lps-defective mice C57BL/10ScCr (Cr) mice carry a
 CC mutation in the IL12RB2 gene leading to the production of a
 CC truncated IL12 receptor beta 2 chain resulting in malfunction of
 CC the IL12-mediated IFN-gamma response.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 2.
 CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
 CC -----
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 CC -----
 CC DR ENBL; U64199; AAB36676.1; ..
 CC DR MGD; MGI:1270861; IL12RB2.
 CC DR InterPro; IPR002996; Cytok_recept_B/g.
 CC DR InterPro; IPR003961; FN III.
 CC DR InterPro; IPR008957; FN III-like.
 CC DR InterPro; IPR003529; Hemtrecept_1302.
 CC DR InterPro; IPR010457; Lep_receptor_Ig.
 CC DR Pfam; PF00041; fn3; 4.
 CC DR Pfam; PF06328; Lep_receptor_Ig; 1.
 CC DR PROSITE; PS50853; FN3; 5.
 CC DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 CC KW Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 874 Interleukin-12 receptor beta-2 chain.
 FT DOMAIN 24 637 Extracellular (Potential).
 FT TRANSMEM 638 658 Potential.
 FT DOMAIN 659 874 Cytoplasmic (Potential).
 FT DOMAIN 137 234 Fibronectin type-III 1.
 FT DOMAIN 240 332 Fibronectin type-III 2.
 FT DOMAIN 334 430 Fibronectin type-III 3.
 FT DOMAIN 435 532 Fibronectin type-III 4.
 FT DOMAIN 533 631 Fibronectin type-III 5.
 FT SITE 321 325 WSXWS motif.
 FT SITE 677 685 Box 1 motif.
 FT MOD_RES 757 757 Phosphotyrosine (Probable).
 FT MOD_RES 804 804 Phosphotyrosine (Probable).
 FT MOD_RES 811 811 Phosphotyrosine (Probable).
 FT CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 169 169 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 179 179 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 224 224 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 252 252 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 279 279 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 287 287 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 323 323 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 391 391 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
 FT MUTAGEN 677 677 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 693 693 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 727 727 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 737 737 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 748 748 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 757 757 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 778 778 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 804 804 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 811 811 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 866 866 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 FT MUTAGEN 874 874 Y->F: No loss of IL12-induced STAT4
 FT activation nor T-cell proliferation. No
 FT effect on IFN-gamma production.
 SQ SEQUENCE 874 AA; 98196 MW; 58254D21BF1BD67 CRC64;
 Query Match 9.4%; Score 328.5; DB 1; Length 874;
 Best Local Similarity 23.0%; Pred. No. 2.9e-13;
 Matches 153; Conservative 91; Mismatches 268; Indels 153; Gaps 32;
 QY 39 LQCYGVGPIGLDNCSEPP-----LGDLCAPSELHLQSKYRSNKTQ----- 79
 DB 143 ISCVQEGENGTVACSWNSGKVTYLTNTYTLQLSGPNNLTCCQCFSDNRQNCNRLDLGIN 202
 QY 80 -TVAAAGRSWVAIPR-EQLTMSDKLLVMGTAGQPLWPPVFNLETQMKPNAPRLGPDV 137
 DB 203 LSPDLAERSFIVRTAINDLGNSSSL-----PHTFTFLDIVIP--LPPWDIRI 248
 QY 138 DFSEDDPLEATVHWAPPTWPSHKVLCQFHYRCQEAATLLPELKTIPLTVPVEIQDLE 197
 DB 249 NFLNASSRGTTLQWE---DEGOVLNQLRYQPLNSTSNMNVN---ATNAKGKYLDRDLR 301
 QY 198 LATGYKVGRCRMEKEEDLWGEWSPILSPOTPPSPAP---KDVN-----VSGNL 242
 DB 302 PFTFEBFQISKLHLGGGSWNSWSESILRTPTPEEPVIGILDIMWKQDIDYDQQIIS--- 358
 QY 243 CGTPGGEELLLWKAQPCQVQSVYKFWVWGGRELSPEGI-----TCCCSLIPSGAEW 295
 DB 359 -----LFWKSLNPSSEARGLIHYQVTLQEVTKTTLQNTTRHTSWTRVIRPTGAW 408
 QY 296 -ARVSANATSWEPNLNLSIV--CLDSASAPRSVAVSSITAGSTELLVTPWOP---GPGEPL 349
 DB 409 TASVSAANSKGASAPTHINIVDLCTGTLGLAPHQVSAS-ENMDNILLVTPWPPKKAUSAVR 467
 QY 350 EHVVDW-ARDGDPLEKL--NWRLPPGNLSALLPGNFTVGVPYRITVTVASGLASASS 406
 DB 468 EYIVENRALQPGSITKFPFPHWLRIIPDNNNSALISSEIKPKYICVIRVHALSES-QGCGSS 526

DR	EMBL; AJ308426; CAC28320.1; -.
DR	HSP; P40189; 1BQU.
DR	GO; GO:0042022; C:interleukin-12 receptor complex; NAS.
DR	GO; GO:0016517; F:interleukin-12 receptor activity; NAS.
DR	InterPro; IPR002996; Cytn recept_B/G.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR003529; Hemtrecept_L102.
DR	InterPro; IPR010457; Lep_receptor_Ig.
DR	Pfam; PF00041; fn3; 3.
DR	Pfam; PF06328; Lep_receptor_Ig; 1.
DR	SMART; SM00060; FN3; 4.
DR	PROSITE; PS00853; FN3; 5.
DR	PROSITE; PS01353; HEMATOPO REC_L_F2; 1.
DR	KW Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
DR	Transmembrane.
KW	SIGNAL 1 23 Potential.
FT	CHAIN 24 861 Interleukin-12 receptor beta-2 chain.
FT	DOMAIN 24 622 Extracellular (Potential).
FT	TRANSHEM 623 643 Potential.
FT	DOMAIN 644 861 Cytoplasmic (Potential).
FT	DOMAIN 124 218 Fibronectin type-III 1.
FT	DOMAIN 224 316 Fibronectin type-III 2.
FT	DOMAIN 317 415 Fibronectin type-III 3.
FT	DOMAIN 420 518 Fibronectin type-III 4.
FT	DOMAIN 521 616 Fibronectin type-III 5.
FT	DOMAIN 750 753 Poly-Pro.
FT	SITE 305 309 WSXWS motif.
FT	SITE 662 670 Box 1 motif.
FT	SITE 800 806 Required for STAT4 binding (By similarity).
FT	CARBOHYD 48 48 N-linked (GlcNAc..)(Potential).
FT	CARBOHYD 129 129 N-linked (GlcNAc..)(Potential).
FT	CARBOHYD 166 166 N-linked (GlcNAc..)(Potential).
FT	CARBOHYD 271 271 N-linked (GlcNAc..)(Potential).
FT	CARBOHYD 347 347 N-linked (GlcNAc..)(Potential).
FT	CARBOHYD 376 376 N-linked (GlcNAc..)(Potential).
QY	SEQUENCE 861 AA; 96208 MW; 487B1E5D1E358E5B CRC64;
Query Match 9.3%; Score 326.5; DB 1; Length 861;	
Best Local Similarity 24.5%; Pred. No. 3.8e-13;	
Matches 171; Conservative 88; Mismatches 281; Indels 157; Gaps 36	
Qy	39 LQCVGVGPLGLNCSWBPLGD-----LGAPSELHLQSQ----- 71
Dd	130 LSCIQKGERGVTCWHGRDRTHLYATVLTQLNGPKNLTWQKCNHDYCDHLDLGINLTP 189
Qy	72 KYRSNT-QTVAVAGRSVAIPREQLTMSDKLLWGCTKAGOLPWPVFVNLETKMPEN 129
Dd	190 ESLESSYTVKVTAISNLGSASSFP-FSGLTDIV-----RPL-PPWDIRIKF----- 234
Qy	130 APRLGPDPDFSEDDPLEATVHWAPPWPDSHKVLICQFHRRRCQEAAWTLLPELKTIPT 189
Dd	235 -----VNASVD---RCTLLWR----DEGLVLLNRLRYRPINSRWNVN---VTNKG 277
Qy	190 PVEIQDLLELATGYKYVGRCKMEKEDLMGEWSPILSFOTPPSAP---KDW-----VSGN 241
Dd	278 RHDLDLKPFFEYEFOISSKLHLKYGSDWSSESRLQTPEEPITGMNVMYMRQHIDYN 337
Qy	242 LCSTPGGEEPLLWK-----APGPCOVQSVKVMFW-VGGRELSPGEGTCCCS---LIPS 291
Dd	338 -----RQIISFLFKWNGLSLSEARGILH--VOYTLQKVGAGEITLQNIHTSWTWVIPR 389
Qy	292 GAEW-ARVASNA--TSWEPTLNLSLVCLDSASAFPSVAVSSIAGSTELLVTWQP---CP 345
Dd	390 TGNWAAAVSAANSKGSSLPRINTDLCGAELLAPOQVLAKS-EGMDKLMVTWTPPEKAT 448
Qy	346 GEPIEHVVWDARDGP-----LEKLNWVELPCNLSALLPGNFTVGPVPYRIITVAVSASGL 401
Dd	449 AAOVEYVYVW-REALHPGAGMQPPLGWLSPTPYRSALISENIKPYICYEIRVHAL-AQGQ 506
Qy	402 ASASSVWGFEELAPLVGFTTLWRLODAPPGTPAIANGEVPRHQLRGHLPHYTLIC---AOS 458

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Db 507 GGCNSTRGNSQKAPLSPGHINAISE-BKGSVLISWDEIPAREOMGCILHYRVIWKERDS 565
Qy 459 GTPSEVC-----MNVSGTQSVTLPLPMGCPCELVWTASTIAGQGGPPGPTILRLHLPDNTLRW 515
Db 566 NSQPOLCEIPVIRISPNHPIBSLQ-PRVTVYVLMWLTALTAAGESPQGNREFFCL-QGRKANW 623
Qy 516 KVLPGILFLWGLFLGCGLSLATSRCVHLRHKL-----PRWWEKVPDPANSSSGQPH 570
Db 624 STFWAPSCINAVIMVG-----VLSMRCPQKVFVLLLRPQWCSKEIPDPANSTWAKY 678
Qy 571 MEQVPEAQPLGDLFILE---VEEMEP-----PP-----VMSSQPAQA--T 606
Db 679 PIVEKTKQLALDRLLTWTPEPEPEPLVINEVLCRVTFVFRPHRHSWSEKGGVQGHYT 738
Qy 607 APLDSGYEKHFLPTP-----EELGLLGP 629
Db 739 SEEDTGYSSASPPPPRAPTAFTGQGVLDLYKVLGSKGP 775

RESULT 8
Q6UANO PRELIMINARY; PRT; 870 AA.
AC Q6UANO;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Class I helical cytokine receptor number 26.
GN Name=CRFA26;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP SEQUENCE FROM N.A.
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blimont C., Skalli Z., Catolico L., Poulain J., Berardinis Vd.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigs R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quirier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Crollius H.R.;
RA "Analysis of the Tetraodon nigroviridis genome reveals the
RT protokaryotype of bony vertebrates and its duplication in teleost
RT fish."
RL Nature 0:0-0(2004).
DR ENBL; AY174498; AAR25689.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS00853; FN3; 3.
KW Receptor.
SQ SEQUENCE 870 AA; 94718 MW; 6322B1618DC3E733 CRC64;

Query Match 8.9%; Score 313; DB 2; Length 870;
Best Local Similarity 22.88; Pred. No. 3e-12;
Matches 151; Conservative 91; Mismatches 263; Indels 156; Gaps 29;

Qy 50 LNCSEWPLGDLGAPSELHLSQKYSRKNKTQVAVA-----GRSWAIPREQLTMSD 101
Db 137 MSCRWDPG-----RQTAAATYTLTVAVRAVSNFVSVGTGRSGVPMVPVFFHM 187
Qy 102 KLLW-----GTAKQPL-----WPPVFVNLETOMKNAP---RLGPPVDFSEDDPLE 146
Db 188 LLDIWVEARNILGTVESQHLQDAGW---FV-----KPPPSSELTILISEKSF-----PTS 234
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Qy 147 ATVHWAPPTWPSHKVLICQPHYRRCCQAAWTLLEPELKTIPTEIQLDELATGYKVG 206
Db 235 LLSQWKHPIASVYVMTLYEIRFRAEADPGWTDVPAADTSKDIESFRLOKLRPDTLYTVQV 294
Qy 207 RCMEKEEDLWGSWSPILSFQTP---PSAPKDVVWSGNLCTPGGEEPLLWKAPGCVQ 263
Db 295 RCKYAHNGLHWSWS-TKATRTPEDKTSRPNWI---VAAKPGDRK-----GKWLQ 342
Qy 264 VSVKWFVWVGRELSPEGITCCCSLIPS-----CAEWARVSANVATSW----- 306
Db 343 VVAKDPKFSNGK-----IOCFEIQSLDEPLRNPGEWERTAVQAAPYDGRHLLK 396
Qy 307 -----EPLTNLSLVCLDSASA-----PRSVAVSSIAG----- 333
Db 397 QLLLPEGLNVSVVAVNSVGASPVASLIIPKRTHGGCGKARRGASTRTVGLCAELPPV 456
Qy 334 -----STELLVTWQPGGEPL-EHVVDWARDGDPLEKLNWVRLPPGNLSALLPNFT 384
Db 457 EDLEVRPRGGRLELRWRPSSWRTASVYVWSSGAG-----WDQRESRGTNTTLRGLD 512
Qy 385 VGVPIRTTAVSASGLASASSVMGFEELAPLVGPTLMELQDAPGCTPA-IANGEVPRH 443
Db 513 RFVCMISVPPYISRRLLGAPGSAQAFLQGALEGPV-AVKDKPGHNEVELVWTEIPAH 571
Qy 444 QLRGHLTHYTLCAQSGTSPSCMNVSGNTQSVTLPLPMG-PCELWVTASTIAGQGGPPG 502
Db 572 QREGFITNYTFYSSD-----ITVAANTSYLSSLSGNTRYDAWVAVSTSAAR--PGA 623
Qy 503 ILRLHLPDNTLRWKLPGILFLWGLFLGCGLSLATSRCYHLRHKLPRWWEKVPDPA 562
Db 624 TTTTSPPTGEVEAIVVVVCLLFFFLV-----LMATLLCIY-KEDTIKSLWPOINPG 677
Qy 563 NSSSG-----QPHWEQVPEAQPLGDLFILEVEEMEPVPMWESSQPAQATAPLSGY--EK 615
Db 678 ESTIGTWAPDYPLKAEPTKDGCVGSVLLAVDVCVQVLEED---KAVLPLKDKYLSEE 734
Qy 616 H 616
Db 735 H 735

RESULT 9
GCSR HUMAN STANDARD; PRT; 836 AA.
AC Q39062;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R)
DE (CD114 antigen).
GN Name=CSF3R; Synonyms=GCSFR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91079757; PubMed=2147944;
RA Larsen A., Davis T., Curtis B.M., Gimpe J.E., Cosman D.,
RA Park L., Sorensen E., March C.J., Smith C.A.;
RT "Expression cloning of a human granulocyte colony-stimulating factor
RT receptor: a structural mosaic of hematopoietin receptor,
RT immunoglobulin, and fibronectin domains."
RL J. Exp. Med. 172:1559-1570(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91062348; PubMed=1701053;
RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;
RT "Three different mRNAs encoding human granulocyte colony-stimulating
RT factor receptor.";
```


FT	CHAIN	25	836	Granulocyte colony stimulating factor receptor.
FT	DOMAIN	25	627	Extracellular (Potential).
FT	TRANSMEM	628	650	Potential.
FT	DOMAIN	651	836	Cytoplasmic (Potential).
FT	DOMAIN	25	117	Ig-like C2-type.
FT	DOMAIN	122	222	Fibronectin type-III 1.
FT	DOMAIN	237	330	Fibronectin type-III 2.
FT	DOMAIN	334	426	Fibronectin type-III 3.
FT	DOMAIN	430	522	Fibronectin type-III 4.
FT	DOMAIN	527	618	Fibronectin type-III 5.
FT	SITE	318	322	WSXWS motif.
FT	SITE	658	666	Box 1 motif.
FT	DISULFID	131	142	By similarity.
FT	DISULFID	248	295	
FT	DISULFID	266	309	
FT	CARBOHYD	51	51	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	93	93	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	128	128	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	134	134	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	389	389	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	474	474	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	579	579	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	610	610	N-linked (GlcNAc. . .) (Potential).
FT	VARSPIC	750	783	VLYQLGSPSPGPGHYLRCDSTQPLLAGLTPS -> AGP
Query Match				8.5%; Score 297.5; DB 1; Length 836;
Best Local Similarity				22.8%; Pred. No. 3.1e-11;
Matches				158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;
Qy	50	LNCSEPLDGLGAPSELHLSQKYSRN-KTQTAVV-----AAGRSWVAIPREQLTMSDKL	103	
Db	140	LICQWEPGPEHPTSLTKSFSGKNCQIQGSDILDCVPKQSGSHCCIPRKHLILQNM	199	
Qy	104	LVW-----GTRAGQPLW-----PPVFNLSTQMKPNAPRLG-----PDVDF	139	
Db	200	GIWVQAEALGTSMSPOLCLDPMVDVKLEPPMLRTMDPSPEAAPQAGCLQLCWEP----	255	
Qy	140	SEDDPLEATVHWAPPTWPSHKVLICQF-HYRRCQEAATLLEPELKTIPLTPTVEIQDEL	198	
Db	256	-----WQGLHINK-----CELRHPQGEASWALVGP-----LPLEALQYEL	294	
Qy	199	-----ATGYKYVGRCRMEKEEDLWGEWSPILSFOTPPSAPK-----DVWVSGNLCTPGGEE	250	
Db	295	CGLLPATAYTLQIRCIWPLPGHSDWSPSLERLTERRATVRLDTW-----	341	
Qy	251	PLLLWKAPGCVQVSYKVFVWVGRELSPGIGITCCCSLIPSGAEWARKVSNATSWEP--	308	
Db	342	-----WRO-----RQLDPRTVQLFWKVPVLEEDSGRIQGY-VVSWRPSG	379	
Qy	309	-----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST-----	335	
Db	380	QAGAILPLCNTELTCTFHLPSBAQEVVALVAYSAGTSRTPVVFSSRGPAITRLHAMA	439	
Qy	336	-----ELAVTWQPGFGEPLHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGP	388	
Db	440	RDPHSLWGVGEPNPWPQGVIEWGLGPPSASNSKTRWMEQNGRATGFLLKENIRPQL	499	
Qy	389	YRITVTAVSAGLASASSVNGFREELAPLVGPTLWRLQDAPGTPATAJWGEVPRHQLRGH	448	
Db	500	YEIIVTPLYQDTWGPSQHVYAYSQEMAPSHAPEL-HLKHIGTKWAQLEWPEPEPELGKSP	558	
Qy	449	LTHVTLCAQSGTSPSCMVNSGNTQSVTLDPWGPCELW-----VTA	491	
Db	559	LTHYITFWNAQNSQFAILNASSRGVPLHGLE--PASLYHIHLMASQAGATNSTVTLT	616	
Qy	492	STIAGQPGPIILRLHLPLDNTLRWKVPLGILFWGLFLL--GGLSLATSGRCYHLRHK	548	
Db	617	MTLTPEG-----ELHI-----ILGLFGLLLLTCLCG-----TAWLCCSPNRK	655	
Qy	549	VLPWRVWKEVPDPANSSG-----OPHMEQVP--EAQPLGDLPILEVEEMEPFPMES	599	
Db	656	-----NPLWPSVDPDAHSSLSGWSVPTIMEBDAFQLPGLGTPTIKTLVLEEKKVPV-WES	711	

Qy	600	SQPAQATAPLDSGYEKHFLPTPELGLL-GPPR	631	
Db	712	HNSSETCG-----LFTLVQTYVLQGDPR	734	
RESULT 10				
Q65214	PRELIMINARY;	PRT;	962	AA.
ID	Q65214			
AC	Q65214			
DT	25-OCT-2004	(TREMBlrel. 28, Created)		
DT	25-OCT-2004	(TREMBlrel. 28, Last sequence update)		
DT	25-OCT-2004	(TREMBlrel. 28, Last annotation update)		
DE	Oncostatin M specific receptor.			
GN	Name=OSMR;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Okaya A., Kitanaka J., Kitanaka N., Satake M., Terada K., Sugiyama T.,			
RA	Takemura M., Fujimoto J., Terada N., Miyajima A., Tsujimura T.;			
RT	"Rat oncostatin M specific receptor mRNA."			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB167522; BAD44758.1; ..			
KW	Receptor.			
SQ	SEQUENCE. 962 AA; 108624 MW; A7A15FED59A6E21A CRC64;			
Query Match				
Best Local Similarity				
Matches				
Query				
Db	50	LNCSEPLDGLGAPSEL--HLQ-SQYR-----SNKTQTVAVAGRSWVAIPREQLTMSD	101	
Qy	251	LNCLEWP-----GIDTTLTSHWKQSRQHYTLYESPSGRREVSNHRNSTWQITDSQETYNF	306	
Db	102	KLLVWGTKAGQPLWPPVFVNLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKV	161	
Qy	307	TLTAENNLKRVS--SISFNLTHRVHPKAPH---DVLTKVTGATKAHMTWKVPSRGDY-T	360	
Db	162	LICQFYRRQCEAAWTLLEPELKTIPLTPTVEIQDELATGKYVGRCRMEKEEDLWGEWS	221	
Qy	361	LLCQVEL-QCE--GEVIHEHNVSVHTSANVLSFDSLEPDIEYKACVRCASANHHKWSDDW	417	
Db	222	PILSFOTPPSAPK---DVWVSGNLCTPGGE-----BPLLLWKAPGCVQVSYKVFVW	271	
Qy	418	Q-KKFTPEAPSEALDVWRD---VRTENGRHVVTFLFWKPLLSQANGKI--ISYNI---	468	
Db	272	VGGRELSP-----GITCCCSLIPSGAEWARKVSNATSWEPITNLSLCLDS	319	
Qy	469	VENEANPTESEQYSVRAPALGNLSLDLHPYK---IHISANNASAGASP---BSLVVLS	522	
Db	320	ASAPRSVAVSSIAAG-STELLVWQPGFGEPLHVVDWARDGDPLE-KLNWVRLPPGNLSA	377	
Qy	523	HSGHEEVHEKTIKIKNGFNISWEPVSGDAIGYVVDWCAHSQTCQRCDLQWKNVGNITST	582	
Db	378	LIPGN-FTVGVPIRVITVAVA-SGLASASSVNGFREELAPLVGPTLWRLQDAPGTPAI	435	
Qy	583	IITSDAFEPGVRYNFRIFERSVEENVRLVEKQGYTQELAPSVNPGV-TIHNLTPNSFSL	641	
Db	436	AM-----GEVPRQLRGLTHY-----TLCAQSGTSPSCMVNSGN	471	
Qy	642	KWQDYASDFQSGFIKGYLVYLSKELQCNPNWERTVLSDKSVLCKYVDVDDP	693	
Db	472	TQSVTLPLDL-PWGPCELWWTASTIAQGGPPGPIILRLHLPLD---NTLRWKVPLGILFWGL	527	

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Db 694 TKTLAVENLRPSLYEFLVTPYTSAGQGNETYTKVTTPDVRSHMLLQIILP----- 745
QY 528 FLGCGLSLATSRCVYHLRHKVLPRWWEK-----VPDPANSS----- 565
Db 746 MTLGVFLSIIV---CYW-----KSNQWKEKCYDPINPNYKSSILSLIKSKNPHLIMNVK 797
QY 566 -----SGOPHMEQVPEAQLGDLPLILEVEEMEPFPPVMESSQPA 603
Db 798 DCIPDVLEINKAEGSKTCVSGKLTEDVTKPPL--VP-TEKDSSGPFVLENFPT 854
QY 604 QATAPLDSGYEKHFLP-----TPBELGLLGGP 630
Db 855 YDQSAFDSG-SHGFTPGPLKNTPHQLGLLAPP 885

RESULT 11
ID O70458 PRELIMINARY; PRT; 971 AA.
AC O70458;
DT 01-AUG-1998 (TREMELrel. 07, Created)
DT 01-AUG-1998 (TREMELrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Oncostatin M specific receptor.
GN Name=Osmr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252923; PubMed=9584176;
RA Lindberg R.A., Juan T.S., Welcher A.A., Sun Y., Cupples R.,
RA Guthrie B., Fletcher F.A.;
RT "Cloning and characterization of a specific receptor for mouse
RT Oncostatin M.";
RL Mol. Cell. Biol. 18:3357-3367(1998).
DR EMBL; AF058805; AAC40122.1; -.
DR MGD; MGI:1330819; Osmr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004924; F:oncostatin-M receptor activity; IDA.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR002996; Cytkn recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003529; Hemtrecept_1302.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 971 AA; 110229 MW; BECA085BBD47C1E7 CRC64;
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Query Match 8.3%; Score 292; DB 2; Length 971;
Best Local Similarity 22.9%; Pred. No. 8.5e-11;
Matches 159; Conservative 87; Mismatches 275; Indels 174; Gaps 34;

QY 50 LNCSEPLDGLAPSELHLQSKYR-----SNKTQVAVAGRSWVAIPREQ----- 96
Db 250 LDCSEWP-----GVDTLTWKRFQNYTLCSFSKRCESVSNYSYTWITGSEQMYNF 305
QY 97 -LTMSDKLLVWGTKAGQPLPVPFVNLETQMPNAPRLGPDVDFSEDDPLEATVHWAPPT 155
Db 306 TLTAENQLKRSVN-----INFNLTHRVHPKAPQ---DVTLKIGATKANWYKVS 354
QY 156 WPSHKVLIQCFHYRRCQEAWLTLELPELKIPLTPVEIQDLELATGYKYVGRCKMEKED 215
Db 355 HGNVYTLCCQVKLQYGE---VTHEHNVSVHMSANYLFSDDLDPDTKYKAFVRCASANHF 410
QY 216 LMGWSPILSFQTPPSAPK---DVWVSGNLGTPGSEEPILLWKAPGCVQ-----VS 265
Db 411 KWSDMTQK-KEFSTPETAPSQALDVG---RQVWSENGRRIVTLFWK---PLLKSOANGKIIS 464
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QY 266 YKVMFWVGRELSPEGITCCCLIPSGAWEA-----RVSAVNATSWEPFL 309
Db 465 YNI---VVENEAKPTSEHYC-----VWAPALSTNLSLDLPYKIRITTNNSMGASP- 513
QY 310 TNLVLVCLDSASAPRSVAVSSIAGSTELL-VTWPGPGCEPLEHVVDW-ARGDDPLEKLNW 367
Db 514 --ESLWLSNDSGHEEVKEKTIKIGKDAFNISWEPVSGDTMGYYVDWCAHSQDQRCDLQW 571
QY 368 VRLPPGNLSALLPG-NFTVGPYRITVTAVSASGLAS-ASSVWGFRFELAPLVGPTLWRL 425
Db 572 KNLGNTTSTTITSDDFKPGVRYNFRIFERSVEHKARLVEKQRTQBLAELVNPKV--- 628
QY 426 QDAPPGTP---AIANGEVPRHQLRHLTHYTLCAQS-----GTSPSCVMN 467
Db 629 -EIPYSTENSFVLWPDYDSDFQAGFIKGYLVVYKSKEMQCQNPWERTLLPDNSVLCKYD 687
QY 468 VSGN-TQSVTLDDL-PWGPCELVWTASTIAGQGGPPIRLHLDPNTLRWKLPGILFLW 525
Db 688 INGSETKLTVENLQPELSLEYEFFVTPTYSAGPGNETFTKVTTPD--ARSHMLLQIILPM 745
QY 526 GLFLGCGLSLATSRCVYHLRHKVLPRWWEK---VPDPANSS----- 565
Db 746 TLCVL---LSIIV---CYW-----KSNQWKEKCYDPINPNYKSSILSLIKSKNPHLIMN 794
QY 566 -----SGOPHMEQVPEAQLGDLPLILEVEEMEPFPPVMESSQ 601
Db 795 VKDCIPDVLEINKAEGSKTCVSGKLTEDVTKPPI--VP-TEKDSSGPFVLENFPT 851
QY 602 PAQATAPLDSGYEKHFL-----TPBELGLLGGP 630
Db 852 FTYDQSAFDSG--SHGLIPGLKDTAHLGLLAPP 884

RESULT 12
O88821
ID O88821 PRELIMINARY; PRT; 970 AA.
AC O88821;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Oncostatin M receptor beta.
GN Name=Osmr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120951; PubMed=9920829;
RA Tanaka M., Hara T., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Miyajima A.;
RT "Reconstitution of the functional mouse oncostatin M (OSM) receptor:
RT molecular cloning of the OSM receptor beta subunit.";
RL Blood 93:804-815(1999).
DR EMBL; AB015978; BAA33725.1; -.
DR MGD; MGI:1330819; Osmr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004924; F:oncostatin-M receptor activity; IDA.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR002996; Cytkn recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003529; Hemtrecept_1302.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 970 AA; 110070 MW; E3A07D41754FA847 CRC64;
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Query Match 8.2%; Score 288.5; DB 2; Length 970;
Best Local Similarity 22.6%; Pred. No. 1.4e-10;

XX	MEDLINE=97331327; PubMed=9187659;
RA	Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
RT	"Solution structure of an extracellular domain containing the WSXWS
RT	motif of the granulocyte colony-stimulating factor receptor and its
RT	interaction with ligand."
EL	Nat. Struct. Biol. 4:498-504(1997).
CC	-1- FUNCTION: Receptor for granulocyte colony-stimulating factor. In
CC	addition it may function in some adhesion or recognition events at
CC	the cell surface.
CC	-1- SUBUNIT: Dimer (Probable).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- TISSUE SPECIFICITY: Found in bone marrow.
CC	-1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC	folding and thereby efficient intracellular transport and cell-
CC	surface receptor binding.
CC	-1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC	activation.
CC	-1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC	Subfamily 2.
CC	-1- SIMILARITY: Contains 5 fibronectin type III domains.
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M58286; AAA37673.1; -.
DR	PIR; A34898; A34898.
DR	PDB; 1CD9; X-ray; B/D=120-334.
DR	PDB; 1CTO; NMR; @=211-333.
DR	PDB; 1GCF; NMR; @=211-333.
DR	PDB; 1PGR; X-ray; B/D/F/H=120-334.
DR	MGD; MGI:1339755; Csf3r.
DR	GO; GO:0030593; P:neutrophil chemotaxis; IMP.
DR	InterPro; IPRO02996; CytKn recept_B/G.
DR	InterPro; IPRO03961; FN_III.
DR	InterPro; IPRO08957; FN_III-like.
DR	InterPro; IPRO03529; Hemtrecept_1302.
DR	InterPro; IPRO10457; Lep_receptor_Ig.
DR	Pfam; PF00041; fn3; 3.
DR	Pfam; PF06328; Lep_receptor_Ig; 1.
DR	PROSITE; PS50853; FN3; 5.
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
DR	3D-structure; Cell adhesion; Glycoprotein; Immunoglobulin domain;
KW	Receptor; Repeat; Signal; Transmembrane.
KW	SIGNAL
FT	1 25 Potential.
FT	CHAIN 26 837 Granulocyte colony stimulating factor
FT	receptor
FT	26 626 Extracellular (Potential).
FT	TRANSNEM 627 650 Potential.
FT	DOMAIN 651 837 Cytoplasmic (Potential).
FT	DOMAIN 26 118 Ig-like C2-type.
FT	DOMAIN 123 223 Fibronectin type-III 1.
FT	DOMAIN 231 328 Fibronectin type-III 2.
FT	DOMAIN 330 429 Fibronectin type-III 3.
FT	DOMAIN 431 525 Fibronectin type-III 4.
FT	DOMAIN 527 621 Fibronectin type-III 5.
FT	SITE 319 323 WSXWS motif.
FT	SITE 658 666 Box 1 motif.
FT	DISULFID 132 143 By similarity.
FT	DISULFID 249 296 By similarity.
FT	DISULFID 267 310 By similarity.
FT	CARBOHYD 51 51 N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 94 94 N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 129 129 N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 186 186 N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 279 279 N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 392 392 N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 408 408 N-linked (GlcNAc. .) (Potential).

FT	CHAIN	26	837	granulocyte colony stimulating factor receptor.
FT	DOMAIN	26	626	Extracellular (Potential).
FT	TRANSMEM	627	650	Potential.
FT	DOMAIN	651	837	Cytoplasmic (Potential).
FT	DOMAIN	26	118	IG-like C2-type.
FT	DOMAIN	123	223	Fibronectin type-III 1.
FT	DOMAIN	231	328	Fibronectin type-III 2.
FT	DOMAIN	330	429	Fibronectin type-III 3.
FT	DOMAIN	431	525	Fibronectin type-III 4.
FT	DOMAIN	527	621	Fibronectin type-III 5.
FT	SITE	319	323	WSXWS motif.
FT	SITE	658	666	Box 1 motif.
FT	DISULFID	132	143	By similarity.
FT	DISULFID	249	296	By similarity.
FT	DISULFID	267	310	By similarity.
FT	CARBOHYD	51	51	N-linked (GlcNAC. . .)
FT	CARBOHYD	94	94	N-linked (GlcNAC. . .)
FT	CARBOHYD	129	129	N-linked (GlcNAC. . .)
FT	CARBOHYD	186	186	N-linked (GlcNAC. . .)
FT	CARBOHYD	279	279	N-linked (GlcNAC. . .)
FT	CARBOHYD	392	392	N-linked (GlcNAC. . .)
FT	CARBOHYD	408	408	N-linked (GlcNAC. . .)

FT	CARBOHYD	474	474	N-linked (GlcNAc. . .)	(Potential)
FT	CARBOHYD	487	487	N-linked (GlcNAc. . .)	(Potential)
FT	CARBOHYD	582	582	N-linked (GlcNAc. . .)	(Potential)
FT	CARBOHYD	613	613	N-linked (GlcNAc. . .)	(Potential)
FT	STRAND	128	135		
FT	TURN	136	139		
FT	STRAND	140	146		
FT	STRAND	156	163		
FT	HELIX	166	188		
FT	STRAND	174	179		
FT	STRAND	186	190		
FT	HELIX	191	193		
FT	TURN	196	197		
FT	STRAND	200	208		
FT	TURN	209	210		
FT	STRAND	211	214		
FT	STRAND	218	220		
FT	HELIX	222	224		
FT	STRAND	226	226		
FT	STRAND	232	235		
FT	STRAND	250	255		
FT	HELIX	258	260		
FT	TURN	261	262		
FT	STRAND	265	273		
FT	TURN	276	277		
FT	STRAND	281	287		
FT	STRAND	290	295		
FT	STRAND	304	312		
FT	STRAND	326	328		
SQ	SEQUENCE	837 AA;	9340 MW;	42295E989E2C8531 CRC64;	
Query Match 7.9%; Score 277; DB 1; Length 837;					
Best Local Similarity 24.2%; Pred. No. 7e-10;					
Matches 172; Conservative 83; Mismatches 295; Indels 162; Gaps 37;					
QY	32	POGSAGPLQCYGVGLDNCSEWPLDGLGAPSELHLSQKYSRN-----KTQTVAAAG	86		
Db	123	PPASPNLSCLMHLTNSLVCQWEPGPEPETHLPSTFILKSFGRADCOYQGDITPCVAKK	182		
QY	87	R-SWVAIPREQLTMSDKLVW-----GKAGQPLW--PPVFNLETKMKNAPRLGPD	136		
Db	183	RONNCISIPRKNLLLYQYMAIWQAEANMLGSSSPKCLDPMVVKLEPML-QALDIGPD	241		
QY	137	VDPSEDDPLEATVHWAPPPTWPSHKVL--ICQFYR-RCQEAATWLL--BPCLKTIPLTPV	191		
Db	242	V--VSHQPGCLWLSWKP--WKPEYMEQECELRYQQLKGANWTLVFLPSSK----	293		
QY	192	EIQDLELATGYKYGRCKMEKEDLNGEWSPILSFOTPPSAPK---DWWVSGNLCGTPCG	248		
Db	294	ELCGLHQAQVYTLQMRGIRSLPGFWSPPGLQRLPRTWKAPTIRLDTWCOKKQL-DPGT	352		
QY	249	EEPLLWKAPGCPVOVSYKWFVW-----GRELSPGEGIT--CCCSLIPSGAEWARV	298		
Db	353	VSQVLFMK-FTPLQEDSGQIQGYLLWNPSDPHQDHLNNTQLSCIFLLPSEAQ----	407		
QY	299	SAVNATSWELTNLSLCLDSA--SAPRSV-----AVSSIAGSTE-----LLVTWQPC	344		
Db	408	-----NVLVAYNKAGTSPTTVVFLNEGPAVTGLHAMAQDLNTIWDWEAP	455		
QY	345	PGEPLEHVVDWARDGDPLEK--LNWRLPPGNLSA-LLPGNFVGVYRITVAVSASGL	401		
Db	456	SLLPQGYLIEWESSPSYNNYSKSMWIEPNNGITGILLKDNINFPQLYRITVAPLYPGIV	515		
QY	402	ASASSVWGPREELAPLVGP-----TLWRLQDAPGTPAIAGVSPRHLRGLHLYHT	453		
Db	516	GPPVNVITFAGEAPPHAPALHLKHVGTWQAQLWEPAPRL--GMIP-----LTHYT	566		
QY	454	L-CAQSGT-SPSVCNVSGNTQSVTLPLD--PWGCELWVTASTIAGQ-GPPGPIRLHLHP	509		
Db	567	IFWADAGHSFVTLNIS--LHDFVLKHELPASLYHVYLMATSRAGSTNSTGLTLATLDP	624		
QY	510	DNTLRWKVLPGLLWGLFLGGLSLATGRCVHLRHKVLPRWVWEKVDPRANS-----	565		

Db	625	SDL-----NIFLGILCLVLLSTTCVTVWLCKRRGKTS----FWSDVDPDPAHSSLSW	673		
QY	566	-----SGOPHMEQVPEAQP-----LGDLPIL---EVEEME	592		
Db	674	LPTMTETQLPSFWDSSVPSITKITELEBEDKPTHWDSESSNGSLPALVQAVVLQGD	733		
QY	593	PPVMESSQPAQATAPLDGSEKHFLLPTBELG-----LLGPPRP	632		
Db	734	PREISNQSPSRGTG--DQVLYGQVLESPTSPGVWQVIRSSTQPLLGPTP	783		
RESULT 14					
IL6B HUMAN					
ID	IL6B HUMAN	STANDARD;	PRT;	918 AA.	
AC	P40189; O9U041;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin				
DE	6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin M				
DE	receptor) (CDw130) (CD130 antigen).				
GN	Name=IL6ST;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Myeloma, and Placenta;				
RX	MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;				
RA	Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;				
RT	"Molecular cloning and expression of an IL-6 signal transducer,				
RT	gp130.";				
RL	Cell 63:1149-1157(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	TISSUE=Synovium;				
RX	MEDLINE=20341529; PubMed=10880057;				
RA	Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,				
RA	Murakami M., Nakao K.;				
RT	"Cloning of novel soluble gp130 and detection of its neutralizing				
RT	autoantibodies in rheumatoid arthritis.";				
RL	J. Clin. Invest. 106:137-144(2000).				
RN	[3]				
RP	PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.				
RX	MEDLINE=21269388; PubMed=11098061; DOI=10.1074/jbc.M009979200;				
RA	Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;				
RT	"Determination of the disulfide structure and N-glycosylation sites of				
RT	the extracellular domain of the human signal transducer gp130.";				
RL	J. Biol. Chem. 276:8244-8253(2001).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.				
RX	MEDLINE=98169383; PubMed=9501088; DOI=10.1093/emboj/17.6.1665;				
RA	Bravo J., Staunton D., Heath J.K., Jones E.V.;				
RT	"Crystal structure of a cytokine-binding region of gp130.";				
RL	EMBO J. 17:1665-1674(1998).				
CC	!- FUNCTION: Signal-transducing molecule. The receptor systems for				
CC	IL6, IL1F, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating				
CC	signal transduction. Binds to IL6/IL6R (alpha chain) complex,				
CC	resulting in the formation of high-affinity IL6 binding sites, and				
CC	transduces the signal. Does not bind IL6. May have a role in				
CC	embryonic development (by similarity). A beta chain.				
CC	!- SUBUNIT: Heterodimer of an alpha and a beta chain.				
CC	!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).				
CC	Secreted (isoform 2).				
CC	!- ALTERNATIVE PRODUCTS:				
CC	Event-Alternative splicing; Named isoforms=2;				
CC	Name=1;				
CC	!- IsoID=P40189-1; Sequence=Displayed;				
CC	Name=2; Synonyms=Gp130-RAPS;				
CC	!- IsoID=P40189-2; Sequence=VSP 001684, VSP 001685;				
CC	!- TISSUE SPECIFICITY: Found in all the tissues and cell lines				
CC	examined. Expression not restricted to IL-6 responsive cells.				

Db 291 TEYVFRIRSIKDSGKGYWDMSEASCTTYEDRSPRPSPFWYKTNPSHGQYRSVRLWK 350
Qy 257 APGPCVQSVYKV-----WFWVGGRELSPE-----GITCC 285
Db 351 AL-PLSEANGKILDYEVILTQSKSVSQTYVTGTTELTNTNDRYVASLAARNKVGKSA 409
Qy 286 CSL-IPSGAEWARVSAVNATSWBPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPG 344
Db 410 AVLTIPSPHVTAAYSVVNLKAF-PKDNL-----LWVEWTPP 444
Qy 345 PGEPLEHVVDWA--RDGDPLEKLNWVRLPCGNLSALLPGNFTVGVYRITVTAVSASGLA 402
Db 445 PKPVSKEYILEMCVLSENAPCVE-DWQOEDATVNRTHLRGRLLSKCYQITVTFVATGPG 503
Qy 403 SASVVMGFRELAPLVGPTLWRLQDAPPGTPATAWGEVPRHQLRGHLTHVTLCAQSGTSP 462
Db 504 GSESLKAYLKQAPARGPTV-RTKKVGKNEAVLAWDQIPVDDQDQGFIRNYSISYRTSVGK 562
Qy 463 SVCNMVSGNTQSVTLPLDPLWGPCELWVTASTIAGQGGPPGPIRLHLP---DNTLRWKVLP 519
Db 563 EMVVHVDSSHTEYTLSSSLSDTLVMVRMAAYTDEGKGDPFTTTPKFAQGEIEAIVP 622
Qy 520 GILPLWGLFLLGGLSLATSGRCVHLRHKVLPRWWEKVPDPDANSSGQ--PH----- 570
Db 623 VCL-----AFLTTLGLVLF--CFNKR-DLIKHIWPNVDPSPKSHIAQWSPHTPPRHN 674
Qy 571 --MEQVPEAQPLGDLPILEVEEMEPPP-----VMES 599
Db 675 NSKDMYSNFTDVSVEIEANNNKPCDDLSVDLFKKEKVSFTEGHSSGIGSSCMSS 734
Qy 600 SQP-----AQATAP-----LDGYEKHFLPT-----PEE 623
Db 735 SRPSSISNEENESAQSTASTVEYSTVHSCY-RHQVPSVQVFSRSESTQPLLDSEERP 793
Qy 624 LGLL 627
Db 794 LQLV 797

Search completed: February 19, 2005, 01:16:02
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: February 19, 2005, 01:07:42 ; Search time 43 Seconds
(without alignments)
1104.112 Million cell updates/sec

Title: US-10-088-950A-1
Perfect score: 3498
Sequence: 1 MRGGRGAPFWLPLKALL.....FLPTPELGLGPPRPQVLA 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	1	US-08-653-740-5
2	3498	100.0	636	2	US-09-073-594-5
3	3498	100.0	636	3	US-09-275-925-5
4	3150	90.1	578	1	US-08-653-740-3
5	3150	90.1	578	2	US-09-073-594-3
6	3150	90.1	578	3	US-09-275-925-3
7	2044	58.4	623	1	US-08-653-740-7
8	2044	58.4	623	2	US-09-073-594-7
9	2044	58.4	623	3	US-09-275-925-7
10	380	10.9	862	2	US-08-685-118-2
11	380	10.9	862	2	US-08-915-495-2
12	380	10.9	862	2	US-08-914-520-2
13	380	10.9	862	4	US-09-853-180B-4
14	380	10.9	864	4	US-09-949-016-7758
15	298.5	8.5	783	6	5422248-2
16	298.5	8.5	783	6	5422248-2
17	297.5	8.5	836	1	US-07-923-976-4
18	294.5	8.4	602	2	US-08-419-652-6
19	292	8.3	863	1	US-07-923-976-8
20	277	7.9	837	1	US-07-923-976-2
21	268.5	7.7	771	1	US-07-923-976-6
22	250	7.1	918	4	US-09-853-180B-3
23	248	7.1	708	1	US-07-797-556-2
24	248	7.1	708	1	US-08-308-881-2
25	248	7.1	708	2	US-09-058-263-2
26	248	7.1	708	2	US-09-059-099-2
27	248	7.1	708	3	US-09-058-264-2

28	248	7.1	708	4	US-09-455-962-2	Sequence 2, Appli
29	248	7.1	708	5	PCT-US95-06530-2	Sequence 2, Appli
30	247	7.1	918	2	US-08-825-558-6	Sequence 6, Appli
31	247	7.1	918	3	US-09-312-611-6	Sequence 6, Appli
32	236.5	6.8	572	2	US-08-419-652-5	Sequence 6, Appli
33	226	6.5	979	1	US-08-308-881-6	Sequence 6, Appli
34	226	6.5	979	2	US-09-058-263-6	Sequence 6, Appli
35	226	6.5	979	2	US-09-059-099-6	Sequence 6, Appli
36	226	6.5	979	3	US-09-058-264-6	Sequence 6, Appli
37	226	6.5	979	4	US-09-455-962-6	Sequence 6, Appli
38	226	6.5	979	5	PCT-US95-06530-6	Sequence 6, Appli
39	217.5	6.2	951	4	US-09-313-942-9	Sequence 9, Appli
40	210	6.0	658	2	US-08-825-558-4	Sequence 4, Appli
41	210	6.0	658	3	US-09-312-611-4	Sequence 4, Appli
42	206.5	5.9	1097	1	US-07-943-843-6	Sequence 6, Appli
43	206.5	5.9	1097	1	US-08-347-003-6	Sequence 6, Appli
44	206.5	5.9	1097	4	US-09-949-016-6209	Sequence 6209, Ap
45	206.5	5.9	1119	4	US-09-949-016-10081	Sequence 10081, A

ALIGNMENTS

RESULT 1
US-08-653-740-5
; Sequence 5, Application US/08653740
; Patent No. 5792850
; GENERAL INFORMATION:
; APPLICANT: James W. Baugartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,740
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-653-740-5

Query Match 100.0%; Score 3498; DB 1; Length 636;
Best Local Similarity 100.0%; Pred. No. 8,1e-280;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGGRGAPFWLPLKALLPLLVLFQTRPGSAGPLQCYGVGPIGLDNCWEPLGDL 60
Db 1 MRGGRGAPFWLPLKALLPLLVLFQTRPGSAGPLQCYGVGPIGLDNCWEPLGDL 60

5,925,735
6,080,406

CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,925
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-275-925-5

Query Match 100.0%; Score 3498; DB 3; Length 636;
Best Local Similarity 100.0%; Pred. No. 8.1e-280;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPLPKLALLPLLVLFQRTTRPGSAGPLQCYGVGLDNCSEWPLGDL 60
DB 1 MRGGRGAPFWLWPLPKLALLPLLVLFQRTTRPGSAGPLQCYGVGLDNCSEWPLGDL 60
QY 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPPV 120
DB 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPPV 120
QY 121 NLETKMPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEA 180
DB 121 NLETKMPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEA 180
QY 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPK 240
DB 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPK 240
QY 241 NLCGTPGGEPLLLWKAAPGCPVQVSVYKFWVWGRELSPGEGITCCCSLIIPSG 300
DB 241 NLCGTPGGEPLLLWKAAPGCPVQVSVYKFWVWGRELSPGEGITCCCSLIIPSG 300
QY 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSVAVSSVAVSSVAVSSVAVSSVAV 360
DB 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSVAVSSVAVSSVAVSSVAVSSVAV 360
QY 361 PLEKLNVRPLPNNLSALLPNNFTVGPYRITVAVSAGSLASSVYMGVGFREELAP 420
DB 361 PLEKLNVRPLPNNLSALLPNNFTVGPYRITVAVSAGSLASSVYMGVGFREELAP 420
QY 421 TLMRLQDAPCTPAIANGVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNGTQSV 480
DB 421 TLMRLQDAPCTPAIANGVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNGTQSV 480
QY 481 PWGCELVWTASTIAGQPGPIRLHLPLPNTLWVKVLPGLIFWGLFLGCGSLATSG 540
DB 481 PWGCELVWTASTIAGQPGPIRLHLPLPNTLWVKVLPGLIFWGLFLGCGSLATSG 540
QY 541 RCVHLRHKVLPRTWKEVPDANSSGQPHMEQVPEAQPLGDLPLILVEEMEPP 600
DB 541 RCVHLRHKVLPRTWKEVPDANSSGQPHMEQVPEAQPLGDLPLILVEEMEPP 600
QY 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

DB 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
RESULT 4
US-08-653-740-3
Sequence 3, Application US/08653740
Patent No. 5792850
GENERAL INFORMATION:
APPLICANT: James W. Baumgartner
APPLICANT: Donald C. Foster
APPLICANT: Frank J. Grant
APPLICANT: Cindy A. Sprecher
TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,740
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-740-3

Query Match 90.1%; Score 3150; DB 1; Length 578;
Best Local Similarity 90.9%; Pred. No. 3.5e-251;
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

QY 1 MRGGRGAPFWLWPLPKLALLPLLVLFQRTTRPGSAGPLQCYGVGLDNCSEWPLGDL 60
DB 1 MRGGRGAPFWLWPLPKLALLPLLVLFQRTTRPGSAGPLQCYGVGLDNCSEWPLGDL 60
QY 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPPV 120
DB 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPPV 120
QY 121 NLETKMPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEA 180
DB 121 NLETKMPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEA 180
QY 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPK 240
DB 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPK 240
QY 241 NLCGTPGGEPLLLWKAAPGCPVQVSVYKFWVWGRELSPGEGITCCCSLIIPSG 300
DB 241 NLCGTPGGEPLLLWKAAPGCPVQVSVYKFWVWGRELSPGEGITCCCSLIIPSG 300
QY 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSVAVSSVAVSSVAVSSVAVSSVAV 360
DB 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSVAVSSVAVSSVAVSSVAVSSVAV 360

Qy	361	PLEKLNWRLPPGNI	SALLPGNFTVGVPYRITVTVA	SSAGLSASASSVWGP	PREBLAPLVP	420
Db	361	PLEKLNWRLPPGNI	SALLPGNFTVGVPYRITVTVA	SSAGLSASASSVWGP	PREBLAPLVP	420
Qy	421	TLWRQDAPP	PGTPTALWGEVPRHQLRGHL	THYTLCAQSGTSPSVMN	SGNTQSVTLPLD	480
Db	421	TLWRQDAPP	PGTPTALWGEVPRHQLRGHL	THYTLCAQSGTSPSVMN	SGNTQSVTLPLD	480
Qy	481	PWGPCELWVTASTI	AGQPPGPIIRLHLPDNTL	RWKVLPGILFLWGLFL	LCGLSLATSG	540
Db	481	PWGPCELWVTASTI	AGQPPGPIIRLHLPDNTL	RWKVLPGILFLWGLFL	LCGLSLATSG	540
Qy	541	RCVHLRHKVLPRW	WEKVPDPANSSGQPHQ	VEAQPGLDPLILEVE	MEBPPVWESS	600
Db	541	RCVHLRHKVLPRW	WEKVPDPANSSGQPHQ	VEAQPGLDPLILEVE	MEBPPVWESS	600
Qy	601	QPAQATAPLDS	GYEKHFLPTPEELGL	GGPPRPQVLA	636	
Db	567	-----	-----GLIGPPRPQVLA	578		

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61	Db	GA	PS	SE	HL	Q	S	K	I	Q	T	V	A	A	G	S	W	V	A	I	P	R	E	Q	L	T	W	S	D	K	L	L	W	G	T	A	G	O	P	L	P	P	V	E	120															
121	Qy	N	L	E	T	O	M	K	N	A	P	R	L	G	D	V	D	F	S	E	D	D	P	L	E	A	T	V	H	A	P	T	W	P	S	H	K	V	L	I	C	O	F	H	R	R	C	O	E	A	A	T	L	L	E	180				
121	Db	N	L	E	T	O	M	K	N	A	P	R	L	G	D	V	D	F	S	E	D	D	P	L	E	A	T	V	H	A	P	T	W	P	S	H	K	V	L	I	C	O	F	H	R	R	C	O	E	A	A	T	L	L	E	180				
181	Qy	P	E	L	K	T	I	P	L	T	P	V	E	I	O	D	L	E	A	T	G	Y	K	Y	G	R	C	M	E	K	E	D	L	W	G	E	S	P	I	S	T	O	T	P	P	S	A	P	K	O	V	W	S	G	240					
181	Db	P	E	L	K	T	I	P	L	T	P	V	E	I	O	D	L	E	A	T	G	Y	K	Y	G	R	C	M	E	K	E	D	L	W	G	E	S	P	I	S	T	O	T	P	P	S	A	P	K	O	V	W	S	G	240					
241	Qy	N	L	C	G	T	P	G	G	E	E	P	L	L	A	K	A	P	C	V	O	V	Y	K	Y	K	W	F	W	G	R	E	L	S	P	E	G	I	T	C	C	S	L	I	P	S	G	A	E	W	A	R	V	S	A	300				
241	Db	N	L	C	G	T	P	G	G	E	E	P	L	L	A	K	A	P	C	V	O	V	Y	K	Y	K	W	F	W	G	R	E	L	S	P	E	G	I	T	C	C	S	L	I	P	S	G	A	E	W	A	R	V	S	A	300				
301	Qy	V	N	A	T	S	W	E	F	L	T	N	L	S	V	C	L	D	S	A	S	A	P	R	S	V	A	S	S	I	A	G	S	T	E	L	L	V	T	W	O	P	G	P	E	L	H	V	V	D	W	A	R	D	G	360				
301	Db	V	N	A	T	S	W	E	F	L	T	N	L	S	V	C	L	D	S	A	S	A	P	R	S	V	A	S	S	I	A	G	S	T	E	L	L	V	T	W	O	P	G	P	E	L	H	V	V	D	W	A	R	D	G	360				
361	Qy	P	L	E	K	N	W	R	L	P	P	G	N	L	S	A	L	L	P	O	N	F	T	V	G	P	Y	R	I	T	T	A	V	S	A	S	G	L	A	S	A	S	V	W	G	F	R	E	L	A	P	L	V	G	P	420				
361	Db	P	L	E	K	N	W	R	L	P	P	G	N	L	S	A	L	L	P	O	N	F	T	V	G	P	Y	R	I	T	T	A	V	S	A	S	G	L	A	S	A	S	V	W	G	F	R	E	L	A	P	L	V	G	P	420				
421	Qy	T	L	W	R	L	O	D	A	P	P	G	T	P	A	I	A	N	G	E	V	P	R	H	O	L	R	G	H	L	T	H	Y	L	C	A	O	S	G	T	S	P	S	V	C	M	N	S	G	N	T	O	S	V	T	L	P	D	L	480
421	Db	T	L	W	R	L	O	D	A	P	P	G	T	P	A	I	A	N	G	E	V	P	R	H	O	L	R	G	H	L	T	H	Y	L	C	A	O	S	G	T	S	P	S	V	C	M	N	S	G	N	T	O	S	V	T	L	P	D	L	480
481	Qy	P	W	G	C	E	L	M	V	T	A	S	T	I	A	G	O	G	P	P	I	L	R	L	H	L	P	D	N	T	L	R	W	K	V																									

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; TELFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 578 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-275-925-3

Query Match      90.1%; Score 3150; DB 3; Length 578;
Best Local Similarity 90.9%; Pred. No. 3.5e-251;
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

Qy 1 MRGGGAPFWLWPLKALLPLLVLFQRTTRPQGSAGPLQCYGVGPGLDLNCNWEPLGDL 60
Db 1 MRGGGAPFWLWPLKALLPLLVLFQRTTRPQGSAGPLQCYGVGPGLDLNCNWEPLGDL 60
Qy 61 GASELHLOKQYRSNKTQTVAVAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVF 120
Db 61 GASELHLOKQYRSNKTQTVAVAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVF 120
Qy 121 NLEQMPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLIQPHYRCQEAATLLE 180
Db 121 NLEQMPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLIQPHYRCQEAATLLE 180
Qy 181 PELXTIPLTVEIQDLDELATGYKYVGRCEMEKEEDLWGEWSPILSFQTPPSAPKDVWVG 240
Db 181 PELXTIPLTVEIQDLDELATGYKYVGRCEMEKEEDLWGEWSPILSFQTPPSAPKDVWVG 240
Qy 241 NLCGTPGGEPLLLWKAFCVQVYKVFVWVGRELSPEGITCCCSLIIPSGAEWAVRSA 300
Db 241 NLCGTPGGEPLLLWKAFCVQVYKVFVWVGRELSPEGITCCCSLIIPSGAEWAVRSA 300
Qy 301 VNATSWPLTNLSLVCLDSASAPRSVAVSSITAGSTELLVTWQPGPGLSHVVDWARGD 360
Db 301 VNATSWPLTNLSLVCLDSASAPRSVAVSSITAGSTELLVTWQPGPGLSHVVDWARGD 360
Qy 361 PLEKLNWVRPPLGNSALLPGNFVTVAVSAGSLASASSVWGFREELAPLVGP 420
Db 361 PLEKLNWVRPPLGNSALLPGNFVTVAVSAGSLASASSVWGFREELAPLVGP 420
Qy 421 TLWRLQDAPGTPAIANGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 480
Db 421 TLWRLQDAPGTPAIANGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 480
Qy 481 PWGCELVWVTAAGTGGPGLRHLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 540
Db 481 PWGCELVWVTAAGTGGPGLRHLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLD 540
Qy 541 RCYHLRHKVLPWWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWVMS 600
Db 541 RCYHLRHKVLPWWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWVMS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 567 -----GLLGPPRPQVLA 578

RESULT 7
US-08-653-740-7
; Sequence 7, Application US/08653740
; Patent No. 5792850
; GENERAL INFORMATION:
;   APPLICANT: James W. Baumgartner
;   APPLICANT: Donald C. Foster
;   APPLICANT: Frank J. Grant
;   APPLICANT: Cindy A. Sprecher
;   TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
;   NUMBER OF SEQUENCES: 42.
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ZymoGenetics, Inc.
;   STREET: 1201 Eastlake Avenue East
;   CITY: Seattle

```

```

; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/653,740
;   FILING DATE:
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Parker, Gary E
;     REGISTRATION NUMBER: 31,648
;     REFERENCE/DOCKET NUMBER: 95-31
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 206-442-6673
;     TELEFAX: 206-442-6678
;   INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 623 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-653-740-7

Query Match      58.4%; Score 2044; DB 1; Length 623;
Best Local Similarity 62.8%; Pred. No. 6.3e-160;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 14 LPKLALLPLLVLFQRTTRPQGSAGPLQCYGVGPGLDLNCNWEPLGDLGAPSELHLOKQY 73
Db 9 LTPLELLLSLMSLLGTRPHGSPGLQCYGVGPGLDLNCNWEPLGDLTETFPVLVHQSKY 68
Qy 74 RSNKTQTVAVAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVFVNLQTKMKNAPRL 133
Db 69 HPNRVWEKVPKQSWVTIPREQLTMSDKLLVWGTAKGQPLWPPVFVNLQTKMKNAPRL 128
Qy 134 GPVDVSEDDPLEATVHAPPTWPSHKVLIQPHYRCQEAATLLEPELKTITPLTVEI 193
Db 129 FSQVDISEATLEATVQWAPPVPPQKALTQPRYKCEQAEATRLPELQKLTPLTVEI 188
Qy 194 QDLLELATGYKYVGRCEMEKEEDLWGEWSPILSFQTPPSAPKDVWVSNLCTGPGEBPL 253
Db 189 QNLEPCTCVQSRCCQVENGYP-WGEWSPILSFQTPFLDPEDEVVSGTVCETSGKRAALL 247
Qy 254 LKAPGFCVQVSYKVFVWVGRELSPEGITCCCSLIIPSGAEWAVRSVAVNATSWPLTNLS 313
Db 248 VMKDPKPCVQVTVVWFGAGDITTTQBEVPCCKSPVPAMWAVVSPGNSTSWVPPTNLS 307
Qy 314 LVCLDSASAPRSVAVSSITAGSTELLVTWQPGPGLSHVVDWARGDPLEKLNWVRP 373
Db 308 LVCLAPESAPCDVGVSSADGSPGIVTKQGTAKPLEYVYVVDWAQDGLDKLWNLRLPPG 367
Qy 374 NLSALLPGNFVTVAVSAGSLASASSVWGFREELAPLVGLTWRLODAPGTP 433
Db 368 NLSTLLPGEFKGGVPYRITVAVYSGLAAPSPVWGFREELVPLAGVAVWRLDDPGTP 427
Qy 434 ATANGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLDPMWGPCELWVTA 493
Db 428 VWANGEVPRHQLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLDPMWGPCELWVTA 487
Qy 494 IACQGGPGLRHLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLDPMWGPCELWVTA 549
Db 488 VACQGGPGLRHLRGLHTHYTLCAQSGTSPVCMNVSGNTQSVTLPLDPMWGPCELWVTA 547
Qy 550 LPEWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWVMSQPAQATPL 609
Db 548 LPQWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWVMSQPAQATPL 604
Qy 610 DSGYKHFPLTPEELGLL 627

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Db      605 YSGYKHFLLPTPEELGLL 622

RESULT 8
US-09-073-594-7
; Sequence 7, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6678
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-073-594-7

Query Match      58.4%; Score 2044; DB 2; Length 623;
Best Local Similarity 62.8%; Pred. No. 6.3e-160;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY      14 LPKLALLPWLVLFORTPOGSGAGPLQCYGVGPLGLNCSWEPLGDLGAPSELHLQSKY 73
Db      9 LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLGTPPVLYHQSKY 68

QY      74 RSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFNLETQMKPNAPRL 133
Db      69 HNRVWEVVKPSKSVTTIPREQFTMADKLLIWTGKGRPLMSSVSVNLETQMKDPTQI 128

QY      134 GPDVDFSEDDPLEATHVWAPPPTWPSHKVLCQFHYRRCQEAATWILLEPDKTIPLTPVEI 193
Db      129 FSQVDISEATEATVQNAAPPVPPVPPKALTQCFRYKECAQEAATWRLPEQLKTDGLTPVEM 188

QY      194 QDELEATGKVGRCRMEKEEDLWGSWSPILGFQTPPSAPKDVWVSGNLCGTPGGEPLL 253
Db      189 QNLEPCTCYQVGRGCVENGYP-WGWSWSPILGFQTPFDVWVSGTVCETSGKRAALL 247

QY      254 LMKAGPCYQVSKYKFWVGGRELSPEGITCCCSLIPSGAEWARVSAVNATSWPEPLTNLS 313
Db      248 WVKDPRPCQVTVTVWFGADITTTQEEVPCCKSPVPAMWENAVVSPGNSTSWVPPTNLS 307

QY      314 LVCLDSASAPRSVAVSSIAGSTELLTWQFGGEPLEHVVDWARDGDPLEKLNWRLPPG 373
Db      308 LVCLAPESAPCDVGVSSADSGSPGIKVTWRQGRKPLEYVVDVAQDGDSDKLNWRLPPG 367

QY      374 NLSALLPGNFTGVGPRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPPGTP 433
Db      368 NLSLLPGEFKGVGPRITVTAVSYGGLAAAPSVMGFREELVPLAGPAVMRLPDDPGTP 427

QY      434 AIANGEVPRHQLRHGLTHYTLCAQSGTSPSCVMNVSGNTQSVTLTLPWGPCELWVTAST 493
Db      428 VVANGEVPRHQLRGQATHYTFCIQSRGLSTVCNVSSQTATLNLHSGSPKLVWTVST 487

QY      494 TAGCGPPGPIRLHLPDNTLRWKLPGILFWGLFLLCGGLSLATS-----GRCYHLRHKV 549
Db      488 VAGQGGPPGDIJSLHLPDNRIRWKLPLWFLSLWGLLLMGGLSLASTRCLQAKCLHWRHKL 547

QY      550 LPRWWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEEMEPFVPMESSQPAQATAPL 609
Db      548 LPQWIEWRVPDPANSSSQPYIKESVLPQPPKDGILVEVEELQPVVES---PRASAPI 604

QY      610 DSGYEKHFLLPTPEELGLL 627
Db      605 YSGYKHFLLPTPEELGLL 622

RESULT 9
US-09-275-925-7
; Sequence 7, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6678
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-275-925-7

Query Match      58.4%; Score 2044; DB 3; Length 623;
Best Local Similarity 62.8%; Pred. No. 6.3e-160;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY      14 LPKLALLPWLVLFORTPOGSGAGPLQCYGVGPLGLNCSWEPLGDLGAPSELHLQSKY 73
Db      9 LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLGTPPVLYHQSKY 68

QY      74 RSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFNLETQMKPNAPRL 133
Db      69 HNRVWEVVKPSKSVTTIPREQFTMADKLLIWTGKGRPLMSSVSVNLETQMKDPTQI 128

QY      134 GPDVDFSEDDPLEATHVWAPPPTWPSHKVLCQFHYRRCQEAATWILLEPDKTIPLTPVEI 193
Db      129 FSQVDISEATEATVQNAAPPVPPVPPKALTQCFRYKECAQEAATWRLPEQLKTDGLTPVEM 188

QY      194 QDELEATGKVGRCRMEKEEDLWGSWSPILGFQTPPSAPKDVWVSGNLCGTPGGEPLL 253
Db      189 QNLEPCTCYQVGRGCVENGYP-WGWSWSPILGFQTPFDVWVSGTVCETSGKRAALL 247

QY      254 LMKAGPCYQVSKYKFWVGGRELSPEGITCCCSLIPSGAEWARVSAVNATSWPEPLTNLS 313
Db      248 WVKDPRPCQVTVTVWFGADITTTQEEVPCCKSPVPAMWENAVVSPGNSTSWVPPTNLS 307

QY      314 LVCLDSASAPRSVAVSSIAGSTELLTWQFGGEPLEHVVDWARDGDPLEKLNWRLPPG 373
Db      308 LVCLAPESAPCDVGVSSADSGSPGIKVTWRQGRKPLEYVVDVAQDGDSDKLNWRLPPG 367

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Db 69 HPNRVNEVUPSKQSWTTPREQFTMADKLLIMQTKGRPLMSSVSNLETSQMKPDPQI 128
Qy 134 GPDVDFEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCOEAAWTLLPELKTIPLTVEI 193
Db 129 FSQVDISEATLEATVQWAPPVWPQKALTCQFRYKECOAEAWTRLEPQLKTDGLTFVEM 188
Qy 194 QDLELATGYKYGRCKMEKEEDLWGEWSPILSPOTPPSAKDVVWSNLCGTGPGGEBPLL 253
Db 189 QNLEPGTCYQVSGRCQVGYGYP-WGEWSSPLSFOTPLDPEDVWVSGTVCETSGKRAALL 247
Qy 254 LWAQPGCVQVSYKVFVWFGRELSREGITCCCSLIPSGAEWARVSAVNAWSEPLTNLS 313
Db 248 VKQDPRECVQVYTVWFAGADITTTQEEVPCCKSPVPAWMEWAVVSGNSTSWPPPTNS 307
Qy 314 LVCLDSASAPRSVAVSSIAGSTELLVWQPGPGEPLHHVVDWARDGDPLEKLNWRLPPG 373
Db 308 LVCLAPESAPCDVGSVADSGPGIKVTWKQTRKPLEYVVDWAQDGLSKLNWRLPPG 367
Qy 374 NLSALLPGNTVGVYPRITVTVASASGLASASSVWGFREELAPLVGTLWRLQDAPPGTP 433
Db 368 NLSTLLPGEFGKGVYPRITVTVASVSGLAAPSVWGFREELVPLAGPAVWRLPDDPPGTP 427
Qy 434 AIWAGEVPRHQLRHLTHYLTCQSGTSPSCVWVSGNTQSVTLPLDPWGPCELWVTAST 493
Db 428 VWAGEVPRHQLRHLTHYLTCQSGTSPSCVWVSGNTQSVTLPLDPWGPCELWVTAST 487
Qy 494 IAGQPGPILRLHLPNTLRWKLPGILFLWGLFLGCGLSLATS---GRCVHLRHKV 549
Db 488 VAGQPGPILRLHLPNTLRWKLPGILFLWGLFLGCGLSLATS---GRCVHLRHKV 547
Qy 550 LPRWVWKVPPDANSNGSGQPHMEQVPEAQPLGDLPILEVEEMPPVPMSSQPAQATAPL 609
Db 548 LPQWIERVEDPANSNGSGQPHMEQVPEAQPLGDLPILEVEEMPPVPMSSQPAQATAPL 604
Qy 610 DSGYKHFLETPBELGLL 627
Db 605 YSGYKHFLETPBELGLL 622

RESULT 10

US-08-685-118-2
; Sequence 2, Application US/08685118
; Patent No. 5840530
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,118
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-685-118-2

Query Match 10.9%; Score 380; DB 2; Length 862;
Best Local Similarity 25.3%; Pred. No. 1.7e-22;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

Qy 31 RPOGSAGPLQCYGVGPIGLDNLCSWEPLGD-----LGAPSELHLSQ----- 71
Db 126 QPON-----LSCIOKSGQGVACTWGERGRDTHLYTEYTLQLSGPKNLWQCKDIYCDYL 181
Qy 72 -----KYRNKTKTV-AVAGRSWVAIPREQLTMSDKLLVWGTAKQPLMPFPVFN 121
Db 182 DFGINLTSPESPENFTAKVTAVNSLSSSLP-STFTFLDIV-----RPL-PPWDIR 231
Qy 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCOEAAWTLLPE 181
Db 232 IKFQ-KASVSR-----CTLYWR-----DEGLVLLNRLRYRPSNLSLNN--- 269
Qy 182 ELXTIPLTPV-----ETDLELATGYKYGRCKMEKEEDLWGEWSPILSPOT---PSAPK 234
Db 270 -----VNVTKAKGRHDLDLKPFTEYEFQISSKLHYKGSWDSSELSRAQTPEEPTGML 325
Qy 235 DVWVSGNLCTPGGEBPLLLWK-----APGPCVQVSYKVFVWFGRELSPE---GITCCC 286
Db 326 DWYMKRHHYD-SRQGISLFWKLSVSEARGKILHYQVTLQELTGKAMTONITGHTSWT 384
Qy 287 SLIPSGAWEA-RVSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVWQ 343
Db 385 TVIPRTGNWAVAVSAANSKGSLLPTRINIMNLCEAGLLAPRQVSANS-EGMDNLTWQ 443
Qy 344 ---GPGEPLEHVVDWAR---DGDPLEKLNWRLPPGNLSALLPGNTVGVYPRITVTVAS 397
Db 444 PRKDPQSAVQYVYVWELHPLPGGTQVPLNWRSPYNVSALISENIKSYCYEIRVYALS 503
Qy 398 ASGLASASSVWGFREELAPLVGTLWRLQDAPGTPAIWAGEVPRHQLRHLTHYLTC--- 455
Db 504 GD-QGCGSSILGNSKHKAPLSGPHINAITE-EKGSILISWNSIPVQEQMGLLHYRIYWK 561
Qy 456 -AQSGTSPSVC---MNVSGNTQSVTLPLDPWGPCELWVTASTIAGQPGPILRLHLPDN 511
Db 562 ERDSNSQPLCEIPYRVSONSHPIINSIQ-PRVTYVLMWLTALTAAGSSHGNEREFCL-QG 619
Qy 512 TLRWK-VLPGI---LFLWGLFLLGCGLSLATSGRVCYHLRHKV-----PRWVWKVP 559
Db 620 KANWMAFVAPSIICIAIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667
Qy 560 DPANSSSGQPH-----MEQVPEAQPLGDLPILEVEEMPPVPMSSQPAQATA-----PLD 610
Db 668 DPANSTCAKKYPIAEKTLQPLDRLLDWPTPS---DPEPLVISEVLHQTVPVFRHPPC 723
Qy 611 SGYKHFLETPBELGLL-----PPRPQVL 635
Db 724 SNWPQ-----REKGIQGHQASEKMMHSSSPPPRAL 756

RESULT 11

US-08-915-495-2
; Sequence 2, Application US/08915495
; Patent No. 5852176
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ

```

; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,495
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-915-495-2

Query Match 10.9%; Score 380; DB 2; Length 862;
Best Local Similarity 25.3%; Pred. No. 1.7e-22;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGAGPQCVCVGLDNLCSWEPLGD-----LGAPSELHLSQ----- 71
Db 126 QPQN-----LSCIQGEQGTACTWGERDTHLYTEYTLQSLGPKNLTWQCKQKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAGRSWVAIPREQLTMSDKLLVMTGKAGQPLWPPVFN 121
Db 182 DFGINLTPESPESNTAKTAVNSLGSSSLP-STFTFLDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHPAPPTWPSHKVLCQPHYRCQBAAWTLLEP 181
Db 232 IKFQ-KASVSR-----CTLVWR-----DEGLVLLNRLRYRPSNRLNM--- 269
QY 182 ELKTIPLTPV-----BIQDLELATGVKYVGRCRMEKEEDLWGEWSPILSFQTP---PSAPK 234
Db 270 -----VNVTKAKGRHDLDLKPFTEYEFQISSKLHLYKGSWSDSLSRAQTPEEPTGML 325
QY 235 DVWVSGNLCTGPGGEEPLLWK-----APGFCVQVSYKVFVWVGRELSPE--GITCCC 286
Db 326 DVWYMKRHIDY-SRQISLFWNLVSEARGKILHYQVTLQELTGKANTQNIHTSWT 384
QY 287 SLIPSGAENA-RVSAVNA--TSWEPLTNLSVLCDLSASAPRSVAVSSVSTAGSTELLVTPQ 343
Db 385 TVIPRTGNWAVASANSKSSLPTRINIMNLCEAGLLAPQVVSANS-EGMDNLTVTQ 443
QY 344 ---GQCEPLEHVVDWAR---DGDPLEKLNWPLPGNLSALLPGNFTVGPVRIYTVAVS 397
Db 444 PRKQPSAVQEVYVREHLPGGDTQVPLNLSRPNVNSALISENIKSYICIEIRVYALS 503
QY 398 ASGLASASVWGFRBELAPLVGPTLRLQDAPPGTPATAWGVPRHQLRGHLTHYTLG-- 455
Db 504 GD-QGCSILGNSKHKAPLSGFHNAITE-EKGSILISWNSIPVQEQMGCLLHYRIYWK 561
QY 456 -AQOSTPSVC---MNVSGNTQSVTLPLDPMWGPBCLWVTASTIAGQPGPPIRLHLPLDN 511
Db 562 ERDSNSQPQLCBIPYRVSNQSHPINSLQ-PRVTYVLLWMTALTAAAGSSHGNERFCL-QG 619
QY 512 TLRWK--VLPGL--LFLWGLFLGGLSLATSGCYHLRHVKV-----PRWVWEKVP 559
Db 620 KANWMAFAPSICIAIMVGIF-----STHYFQQKVFVLLAALRPQWCSEIRP 667

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QY 560 DPANSSQGP-----MEQVPEAOPGLDPLILEVEEMBPVPMVMESSQPAQATA-----PLD 610
Db 668 DPANSTCAKYPVIAEEKTQLPLDRLLIDWPTE-----DPEPLVISEVLHQLVTPVFRHPC 723
QY 611 SGYEKHFLLPTEELGLLG-----PPRPQVL 635
Db 724 SNWPQ-----REKGIQGHQASEKDMHMSASSPPPPRAL 756

RESULT 12
US-08-914-520-2
; Sequence 2, Application US/08914520
; Patent No. 591903
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A.
; APPLICANT: Presky, David H.
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,520
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-914-520-2

Query Match 10.9%; Score 380; DB 2; Length 862;
Best Local Similarity 25.3%; Pred. No. 1.7e-22;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGAGPQCVCVGLDNLCSWEPLGD-----LGAPSELHLSQ----- 71
Db 126 QPQN-----LSCIQGEQGTACTWGERDTHLYTEYTLQSLGPKNLTWQCKQKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAGRSWVAIPREQLTMSDKLLVMTGKAGQPLWPPVFN 121
Db 182 DFGINLTPESPESNTAKTAVNSLGSSSLP-STFTFLDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHPAPPTWPSHKVLCQPHYRCQBAAWTLLEP 181
Db 232 IKFQ-KASVSR-----CTLVWR-----DEGLVLLNRLRYRPSNRLNM--- 269
QY 182 ELKTIPLTPV-----BIQDLELATGVKYVGRCRMEKEEDLWGEWSPILSFQTP---PSAPK 234
Db 270 -----VNVTKAKGRHDLDLKPFTEYEFQISSKLHLYKGSWSDSLSRAQTPEEPTGML 325
QY 235 DVWVSGNLCTGPGGEEPLLWK-----APGFCVQVSYKVFVWVGRELSPE--GITCCC 286

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```
Db 234 IKFO-KASVSR-----CTLYR-----DEGLVLRRLRYRPSNRLWNM--- 271
Qy 182 ELKTIPLTPV-----BIQDLELATGYKVCRCRMEKEEDLWGEWSFILSFQTP---PSAPK 234
Db 272 ----VNVTKAKGRHLLDLKPTEYEFQISSKHLHYKGSWSWSLSRAQTPEEPTGML 327
Qy 235 DVWVSGNLCTPGGEPLLLWK-----APGPCVQVSVKVFVWVGRELSPE--GITCC 286
Db 328 DWYMKRHDY-SRQOISLFWKNLSVSEARGKILHYQVTLQBLTGKANTQITGHTSWT 386
Qy 287 SLIPSGAWA-RVSAVNA--TSWEPLTNLSVCLDSASAPRSVAVSSIAGSTELLVTWQP 343
Db 387 TVIPRTGNWAVASAANSKGSLSLPTRNIMNCEAGLLAPROVSANS-EGMDNILVTWQP 445
Qy 344 ---GPGEPLEHVVDWAR---DGDPLEKLNWRLPQGNLSALLPGNFTVGPVYRITVAVS 397
Db 446 PRKDFSAVQEVYVWRELPBGDQVPLNWLRSRPNVNSALISENISKSYICIEIRVYALS 505
Qy 398 ASGLASASVWGFREELAPLVGPTLWRLQDAPGTPAIAGVPRHOLRGHLHTVTLG-- 455
Db 506 GD-QGCSILGNSKHALSPGHINAITE-EKGSILISWNSIPVOEQMGCLLHYRIYWK 563
Qy 456 -AQSGTSPVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGOGPPGPIRLHLDPN 511
Db 564 ERDSNSQOLCEIPYRVSONSHPIINSLO-PRVTYVLMWTALTAAAGSSHGNERFCL-QG 621
Qy 512 TLRWK--VLPGI--LFLWGLFLGCLSLATSGRCYHLRHVKUL-----PRWWEKVP 559
Db 622 KANWFAVAPSICIAIMVGIF-----STHYFQOQVFLVLLAALRPQWCSEIP 669
Qy 560 DPANSSSGOPH-----MEQVPEAQPLGDLPILEVEEMEPVWESSQPAQATA----PLD 610
Db 670 DPANSTCAKKYIAEKTQPLDRLLIDWPTPE---DPEPLVISEVLHQVTPVFRHPPC 725
Qy 611 SGYERHFLPTPEELGLG-----PPRPQVL 635
Db 726 SNWPQ-----REKGIQGHQASEKDMHMSASPPPPRAL 758

RESULT 15
5422248-2
; Patent No. 5422248
; APPLICANT: SMITH, CRAIG A.; LARSEN, ALF D.; SIMS, JOHN E.;
; BENSON, CURTIS M.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING GRANULOCYTE-COLONY
; STIMULATING FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/6,183
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 587,329
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 522,952
; FILING DATE: 03-APR-1990
; APPLICATION NUMBER: 416,306
; FILING DATE: 03-OCT-1989
; APPLICATION NUMBER: 412,816
; FILING DATE: 26-SEP-1989
; SEQ ID NO:2
; LENGTH: 783
5422248-2
```

```
Query Match      8.5%; Score 298.5; DB 6; Length 783;
Best Local Similarity 23.5%; Pred. No. 7.8e-16;
Matches 164; Conservative 77; Mismatches 259; Indels 197; Gaps 34;

Qy 50 LNCSEPLDGLGAPSELHLSQKYSRN-KTQTVAV-----AAGRSWAIPREQLTMSDKL 103
Db 140 LICOMEPGPEETHLFTSLFKFSKRGNCOTQGDSDLDVCKPQDQGHCCIPRKHLLLYQNM 199
Qy 104 LVW-----GKAGQPLW-----PPVFVNLETQMKFNAPRLG-----PDVDF 139
```

```
Db 200 GIWQAEALGTSMSPOLCLDPMVVKLEPPMLRTMDPSPEAAPQAGCLOLCMEP----- 255
Qy 140 SEDDPLEATVWAPPTWPSHKVILCOF-HYRRCQEAANTLLEPELKTITPLTPVEIQDLEL 198
Db 256 -----WQPGHLHNQK---CELHKPQGEASWALVGP-----LPLEALQVEL 294
Qy 199 -----ATGYKVVGRCRMEKEEDLWGEWSFILSFOTPPSAPK---DVWVSGNLCTPGGEE 250
Db 295 CGLLPATAYTILQIRWPLFGHWSDNSPSELRITERAPTIVRLDTHWRQRL-----D 348
Qy 251 P---LLLKAPCPQVQSVKVMFWVGGRELSPEGITCCSLIPSGAEWARVAVNATSWE 307
Db 349 PRTVQLFWK-FVPLEEDSGRIQGVV-----VSWRPSQAGAILPLCMNTTELS 394
Qy 308 PLTNL-----SLVCLDSA--SAPRSVAVSSIAGST-----ELLVTWQPGP 346
Db 395 CTFHLPSAEQVALVAYNSAGTSRPTPVVFSRGPALTRLHAMARDPHSLWVGMEPPNP 454
Qy 347 EPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGVYRITVTVAVSAGLAS 403
Db 455 WPGVVIWGLGPPSASNSKTWMEQNGRATGFLLENIRPFQLYEIIIVTPIQDTWGP 514
Qy 404 ASSVMGFREELAPLVGPTLWRLQDAPGTPAIAGVEPRHOLRGHLHTYTLCAOSGTSPS 463
Db 515 SQHVYVAYSQEMAPSHAPEL-HLKHHIGKTAQLEWVPEPELKGKPLTHYTIFFWTNAQNS 573
Qy 464 VCMNVSGNTQSVTLPLDLPWGPCELW-----VTASTIAGOGPPGPIRL 506
Db 574 FSAILNASSRGGFVLHGLE--PASLYHILMAASQAGATNSTVLTMLTLPES-----EL 626
Qy 507 HLPDNTLRWKVLPGLIFLWGLFL--CCGLSLATSGRCYHLRHVKVLPWVWEKVPDPAN 563
Db 627 HI-----ILGFLGILLLTCLCG-----TAWLCCSPNRK--NPLWPSVPDPAH 667
Qy 564 SSSG-----QPHMEQVP--EAQPLGDLPILEVEEMEP-- 595
Db 668 SSLGSWVPTIMEEDAFOLPGLGTPITKLTVLEEDKKFVPWESHNSSETCGLPTLVQTY 727
Qy 596 VMESQPAQATAP-LDSGYEKHFUPTPEELGLGPPR 631
Db 728 VLQGDPRAVSTQPOSQSG-----TSDQ---AGPPR 754
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Search completed: February 19, 2005, 01:17:41
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 19, 2005, 01:03:05 ; Search time 175 Seconds
(without alignments)
1405.598 Million cell updates/sec

Title: US-10-088-950A-1
Perfect score: 3498
Sequence: 1 MRGRGAPFWLPLKALL.....FLTPBELGLLGP RPQVLA 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	2 AAW33399	Aaw33399 Alternati
2	3498	100.0	636	4 AAG65270	Aag65270 Cell fact
3	3498	100.0	636	4 AAU01853	Aau01853 Human typ
4	3498	100.0	636	7 ADD68151	Add68151 Human WSX
5	3498	100.0	636	7 ADL26574	Adl26574 Human WSX
6	3498	100.0	636	8 ADL91801	Adl91801 Human PRO
7	3498	100.0	636	8 ADL14163	Adl14163 Human NF-
8	3494	99.9	636	5 ABG32294	Abg32294 Human IL-
9	3494	99.9	636	6 ABU09752	Abu09752 Human T-c
10	3494	99.9	636	6 ABG75880	Abg75880 Human int
11	3490	99.8	636	2 AAY23781	Aay23781 Human DNA
12	3316	94.8	604	4 AAG65271	Aag65271 Cell fact
13	3288	94.0	680	6 ABR41219	Abr41219 Human DIT
14	3150	90.1	578	2 AAW33398	Aaw33398 Human hae
15	3007	86.0	558	8 ADO26826	Ado26826 Human rec
16	2875	82.2	523	2 AAY23785	Aay23785 Partial h
17	2044	58.4	623	2 AAW33400	Aaw33400 Mouse hae
18	2044	58.4	623	4 AAU01854	Aau01854 Mouse typ
19	86.5	25.3	246	2 AAY23786	Aay23786 Partial m
20	415	11.9	82	8 ADR20046	Adr20046 Human imm
21	412	11.8	77	7 ADB36344	Adb36344 Human imm
22	400	11.4	150	2 AAY23782	Aay23782 Mouse DNA
23	380	10.9	862	2 AAW12771	Aaw12771 Human int
24	380	10.9	862	7 ADE39704	Ade39704 Human int
25	380	10.9	862	7 ADF76395	Adf76395 Novel hum

26	380	10.9	862	8 ADK90609	Adk90609 Human IL-
27	380	10.9	862	8 ADM33832	Adm33832 Human IL-
28	380	10.9	862	8 ADO19580	Ado19580 Human PRO
29	380	10.9	862	8 ADP54649	Adp54649 Human PRO
30	331	9.5	861	5 ABB78097	Abb78097 Amino aci
31	330	9.4	861	5 ABB78098	Abb78098 Amino aci
32	298.5	8.5	783	2 AAR11741	Aar11741 Granulocy
33	298.5	8.5	783	2 AAR77868	Aar77868 Human gra
34	298.5	8.5	783	2 AAW10485	Aaw10485 Human gra
35	297.5	8.5	800	2 AAW10486	Aaw10486 Human gra
36	297.5	8.5	801	2 AAR11742	Aar11742 Clone 25-
37	297.5	8.5	813	3 AAB03873	Aab03873 Human gra
38	297.5	8.5	836	2 AAR14255	Aar14255 Human GCS
39	297.5	8.5	836	6 ABU89749	Abu89749 Protein d
40	297.5	8.5	836	8 ADP12979	Adp12979 Protein d
41	297.5	8.5	836	8 ADP44071	Adp44071 Human CSF
42	297.5	8.5	836	8 ADQ59672	Adq59672 Human GCS
43	297.5	8.5	836	8 ADQ60159	Adq60159 Human gra
44	297.5	8.5	836	8 ABM80066	Abm80066 Tumour-as
45	297.5	8.5	836	8 ADP23580	Adp23580 PRO poly

ALIGNMENTS

RESULT 1
AAW33399
ID AAW33399 standard; protein; 636 AA.
AC AAW33399;
XX
XX 22-MAY-1998 (first entry)
XX
XX Alternatively spliced Zcytor1.
XX Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;
KW cancer diagnosis; agonist; antagonist; alternatively spliced.
XX Homo sapiens.
XX
XX WO9744455-A1.
XX
XX 27-NOV-1997.
XX
XX 19-MAY-1997; 97WO-US008502.
XX
XX 23-MAY-1996; 96US-00653740.
XX (ZYMO) ZYMOGENETICS INC.
XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
WPI; 1998-018509/02.
N-PSDB; AAT94120.
Haematopoietic cytokine receptor - useful for ligand detection, and
pathological condition diagnosis.
Claim 7; Page 46-51; 86pp; English.
The present sequence is an alternatively spliced human haematopoietic
cytokine receptor Zcytor1, useful for ligand detection, and pathological
condition diagnosis, including cancer. Receptor agonists of the protein
can be used to stimulate the proliferation and development of target
cells in vitro and in vivo. The agonists can stimulate cell mediated
immunity and lymphocyte proliferation, to treat infection involving
immunosuppression, e.g. viral infections. They may also be used to
suppress tumours, induce cytotoxicity, treat leukopaenias and enhance the
regeneration of the T-cell repertoire after bone marrow transplantation.
Antagonists of the protein may be used to suppress the immune system,
treat autoimmune diseases, including rheumatoid arthritis, multiple
sclerosis and diabetes mellitis. Immune suppression caused by the
antagonists can also be used to reduce rejection of tissue or organ

CC transplants and grafts, and to treat T-cell specific leukaemias and
CC lymphomas
XX
SQ Sequence 636 AA;

Query Match 100.0%; Score 3498; DB 2; Length 636;
Best Local Similarity 100.0%; Pred. No. 8.1e-265;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGGAPFWLWPLKALLPLWVLFORTPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
DB 1 MRGGGAPFWLWPLKALLPLWVLFORTPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
QY 61 GAPSELHLQSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVVF 120
DB 61 GAPSELHLQSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVVF 120
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180
DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180
QY 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
DB 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
QY 241 NLCGTPGGEEPLLWKAPGCPQVQSVYKVFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300
DB 241 NLCGTPGGEEPLLWKAPGCPQVQSVYKVFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300
QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVIAGSTELLVTWQPGGEPLEHVVDWARDGD 360
DB 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVIAGSTELLVTWQPGGEPLEHVVDWARDGD 360
QY 361 PLEKLNWVRLPQNLISALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420
DB 361 PLEKLNWVRLPQNLISALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420
QY 421 TLWRLQDAPPGTPIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLDPDL 480
DB 421 TLWRLQDAPPGTPIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLDPDL 480
QY 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLMGFLGCGLSLATSG 540
DB 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLMGFLGCGLSLATSG 540
QY 541 RCYHLRHVKVLPWVWEKVPDPANSSGQPHMEQVPEAQPLGDLPLILEVEEMEPVPMESS 600
DB 541 RCYHLRHVKVLPWVWEKVPDPANSSGQPHMEQVPEAQPLGDLPLILEVEEMEPVPMESS 600

RESULT 2

AAG65270
ID AAG65270 standard; protein; 636 AA.

XX AC AAG65270;

XX DT 20-NOV-2001 (first entry)

XX DE Cell factor receptor CRL1.

XX KW Cell factor receptor; CRL1; gp130; cancer; inflammation;

XX KW immunological rejection.

XX OS Unidentified.

XX PN CN1299828-A.

XX PD 20-JUN-2001.

RESULT 3

PF 16-DEC-1999; 99CN-00124269.
PR 16-DEC-1999; 99CN-00124269.
XX (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.
XX Cao X, Zhang W, He L;
PI WPI; 2001-523189/58.
DR N-PSDB; AAH79286.
XX
PT New cell factor acceptor, its code sequence and use.
PS Claim 1; Page 19; 27pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of a
CC novel cell factor receptor, designated CRL1. This is a homogeneous
CC molecule of gp130. The sequences can be used in the treatment of cancer,
CC inflammation and immunological rejection. The present sequence is the
CC protein of the invention
XX
SQ Sequence 636 AA;

Query Match 100.0%; Score 3498; DB 4; Length 636;
Best Local Similarity 100.0%; Pred. No. 8.1e-265;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGGAPFWLWPLKALLPLWVLFORTPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
DB 1 MRGGGAPFWLWPLKALLPLWVLFORTPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
QY 61 GAPSELHLQSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVVF 120
DB 61 GAPSELHLQSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVVF 120
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180
DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180
QY 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
DB 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
QY 241 NLCGTPGGEEPLLWKAPGCPQVQSVYKVFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300
DB 241 NLCGTPGGEEPLLWKAPGCPQVQSVYKVFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300
QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVIAGSTELLVTWQPGGEPLEHVVDWARDGD 360
DB 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVIAGSTELLVTWQPGGEPLEHVVDWARDGD 360
QY 361 PLEKLNWVRLPQNLISALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420
DB 361 PLEKLNWVRLPQNLISALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420
QY 421 TLWRLQDAPPGTPIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLDPDL 480
DB 421 TLWRLQDAPPGTPIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLDPDL 480
QY 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLMGFLGCGLSLATSG 540
DB 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLMGFLGCGLSLATSG 540
QY 541 RCYHLRHVKVLPWVWEKVPDPANSSGQPHMEQVPEAQPLGDLPLILEVEEMEPVPMESS 600
DB 541 RCYHLRHVKVLPWVWEKVPDPANSSGQPHMEQVPEAQPLGDLPLILEVEEMEPVPMESS 600
QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636
DB 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636

PT New isolated polynucleotides and polypeptides associated with NF-kappaB
PT pathway, useful for diagnosing, treating, or preventing disorders or
PT diseases associated with NF-kappaB pathway.
XX
PS Claim 6; SEQ ID NO 164; 237pp; English.
XX
CC This invention relates to the novel association of protein sequences (and
CC the genes which encode them) to the NF-kappaB pathway. The invention may
CC be useful for the production of compounds with an anti-inflammatory,
CC cytosolic, hepatotropic, virucide, antiarthritic, antirheumatic,
CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
CC vulnary activity or for gene therapy. The proteins and nucleotides are
CC useful for diagnosing, preventing, treating, or ameliorating conditions
CC or diseases associated with the NF-kappaB pathway. The condition is an
CC immune disorder, an inflammatory disorder, an inflammatory disorder
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
CC immune activity, disorders related to aberrant acute phase responses,
CC organ transplant rejection, conditions related to organ transplant
CC rejection, disorders related to aberrant signal transduction,
CC proliferating disorders, cancers and HIV propagation in cells infected
CC with other viruses. The present sequence is that of a human protein which
CC is subject to the novel association with the NF-kappaB pathway of the
CC invention. Note: This sequence does not appear in the specification but
CC was obtained by the indexer from Genbank.

XX SQ Sequence 636 AA;

Query Match 100.0%; Score 3498; DB 8; Length 636;
Best Local Similarity 100.0%; Pred. No. 8.1e-265;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPKLALLPLLVLFORTPQGSAGPLQCYGVGLDNCSEWPLGDL 60
DB 1 MRGGRGAPFWLWPKLALLPLLVLFORTPQGSAGPLQCYGVGLDNCSEWPLGDL 60
QY 61 GASELHLSQOKRSNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKQPLWPFV 120
DB 61 GASELHLSQOKRSNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKQPLWPFV 120
QY 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCQHYRRCQEAATLLE 180
DB 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCQHYRRCQEAATLLE 180
QY 181 PELKTIPLTVEIQDLATGYKYGRCEKEEDLWGEWSPILSPOTPPSAPKDWVWSG 240
DB 181 PELKTIPLTVEIQDLATGYKYGRCEKEEDLWGEWSPILSPOTPPSAPKDWVWSG 240
QY 241 NLCTPGGEPFLWLKAPGCVQVYKFWVWGRELSPGICCCSLIPSGAEWARSVA 300
DB 241 NLCTPGGEPFLWLKAPGCVQVYKFWVWGRELSPGICCCSLIPSGAEWARSVA 300
QY 301 VNATSWEPFLNLSLVCLDSASAPRSVAVSSVSIAGSTELLVTVQPGFPLEHVVDWARDGD 360
DB 301 VNATSWEPFLNLSLVCLDSASAPRSVAVSSVSIAGSTELLVTVQPGFPLEHVVDWARDGD 360
QY 361 PLEKLNWRLPPGNLSALLPQNFTVGPYRITVAVSASGLASASSVWGFEELAPLVGP 420
DB 361 PLEKLNWRLPPGNLSALLPQNFTVGPYRITVAVSASGLASASSVWGFEELAPLVGP 420
QY 421 TLWLQDAPCTPAIANGEVPRHOLRGHLTHYTLCAOSGTSVSPVCMVNSGNTQSVTLPLD 480
DB 421 TLWLQDAPCTPAIANGEVPRHOLRGHLTHYTLCAOSGTSVSPVCMVNSGNTQSVTLPLD 480
QY 481 PWGPCELWVTASTIAGQPGPILRLHLPNTLRLWVKVLPGLFLWGLFLGCGLSLATSG 540

DB 481 PWGPCELWVTASTIAGQPGPILRLHLPNTLRLWVKVLPGLFLWGLFLGCGLSLATSG 540
QY 541 RCYHLRHKLVRWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEWEPVWVWESS 600
DB 541 RCYHLRHKLVRWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEWEPVWVWESS 600
QY 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVLA 636
DB 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVLA 636

RESULT 8
ABG32294

ID ABG32294 standard; protein; 636 AA.

XX AC ABG32294;

XX DT 10-DEC-2002 (first entry)

XX DE Human IL-12R-like subunit protein.

XX KW IL-D80; human; cytokine; anti-inflammatory; haematopoietic; interleukin;

XX KW IL-27; haematopoietic cell; immune system; inflammation;

XX KW IL-12R-like subunit; interleukin 12 receptor like subunit.

XX OS Homo sapiens.

XX PN WO200268596-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-US005493.

XX PR 22-FEB-2001; 2001US-00791497.

XX PR 30-NOV-2001; 2001US-00000776.

XX PA (SCHE) SCHERING CORP.

XX PI Timans JC, Pflanz SK, Kastelein RA, Bazan JF, Rennick D;

XX PI Dewaal Malefyt R, Cheung J;

XX DR WPI; 2002-706978/76.

XX DR N-PSDB; ABS54548.

XX PT New polynucleotide and its encoded antigenic polypeptide (IL-D80
PT cytokine), useful for regulating hematopoietic cells, in developing new
PT therapies, or for diagnosing or treating abnormal physiology, e.g.
PT inflammations.

XX PS Claim 24; Page 72-74; 74pp; English.

XX CC This invention relates to the DNA and protein sequences of a new cytokine
CC IL-D80. The protein of the invention may have antiinflammatory activity
CC and may act as an IL-D80 modulator or an IL-27 modulator. The
CC polynucleotide of the invention or its encoded polypeptide is useful for
CC regulating the activation, development, differentiation or function of
CC various cell types, e.g. haematopoietic cells. This polynucleotide or
CC polypeptide is also useful in discovering and developing new lymphokines
CC and their related receptor or receptor subunits, and in developing new
CC therapies for a wide range of degenerative or abnormal conditions, which
CC (in)directly involve the immune system or haematopoietic cells. The
CC polynucleotide or polypeptide is useful in diagnosing or treating
CC abnormal physiology or development, e.g. inflammations. The present
CC sequence represents the human interleukin 12- receptor-like subunit
CC protein of the invention

XX SQ Sequence 636 AA;

Query Match 99.9%; Score 3494; DB 5; Length 636;
Best Local Similarity 99.8%; Pred. No. 1.7e-264;
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPKLALLPLLWVLFQRTTRPQSGAGPLQCYGVGGLDNCWSEPLGDL 60
 DB |||||
 QY 1 MRGGRGAPFWLWPKLALLPLLWVLFQRTTRPQSGAGPLQCYGVGGLDNCWSEPLGDL 60
 DB |||||
 QY 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPVPV 120
 DB |||||
 QY 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPVPV 120
 DB |||||
 QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHYRRCOEAAWTLLE 180
 DB |||||
 QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHYRRCOEAAWTLLE 180
 DB |||||
 QY 181 PELKTIPLTPVEIQDELEATGYKVCRCMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
 DB |||||
 QY 181 PELKTIPLTPVEIQDELEATGYKVCRCMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
 DB |||||
 QY 241 NLCGTPGGEPLLLWKAPGCVQVSKYKFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300
 DB |||||
 QY 241 NLCGTPGGEPLLLWKAPGCVQVSKYKFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300
 DB |||||
 QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVGGRELSPEGITCCCSLIPSGAEWARVSA 360
 DB |||||
 QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVGGRELSPEGITCCCSLIPSGAEWARVSA 360
 DB |||||
 QY 361 PLEKLNWVRLPGNLSALLPGNFTVGVYRITVAVSAGSLASASVWGFREELAPLVGP 420
 DB |||||
 QY 361 PLEKLNWVRLPGNLSALLPGNFTVGVYRITVAVSAGSLASASVWGFREELAPLVGP 420
 DB |||||
 QY 421 TLWRLQDAPPGTPTAANGVPRHQRHGLTHYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480
 DB |||||
 QY 421 TLWRLQDAPPGTPTAANGVPRHQRHGLTHYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480
 DB |||||
 QY 481 PWGPCELWVTASTIAGQGPPIRLHLPLDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
 DB |||||
 QY 481 PWGPCELWVTASTIAGQGPPIRLHLPLDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
 DB |||||
 QY 541 RCYHLRHKVLPKRWVKEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPMPVMESS 600
 DB |||||
 QY 541 RCYHLRHKVLPKRWVKEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPMPVMESS 600
 DB |||||
 QY 601 QPAQATAPLDSGYEKHFLTPBELGLLGPFPQVLA 636
 DB |||||
 QY 601 QPAQATAPLDSGYEKHFLTPBELGLLGPFPQVLA 636
 DB |||||

RESULT 9
 ABU09752
 ID ABU09752 standard; protein; 636 AA.
 AC ABU09752;
 DT 07-JUL-2003 (first entry)
 DE Human T-cell cytokine receptor (TCR).
 KW Human; interleukin; IL-D80; IL-D80; DNAX; immunosuppressive;
 KW antiinflammatory; cardiant; nootropic; neuroprotective; gene therapy;
 KW antigen; cell activation; cell development; cell differentiation;
 KW haematopoietic cell; immune disorder; T-cell immune deficiency;
 KW inflammation; tissue rejection; cardiovascular disorder; TCCR;
 KW neurophysiological condition; immunological condition; receptor;
 KW Epstein barr virus induced gene 3; EB13; T-cell cytokine receptor.
 OS Homo sapiens.
 XX US2003008343-A1.
 PN 09-JAN-2003.
 PD 22-FEB-2001; 2001US-00791497.
 PF 30-JUL-1999; 99US-0146581P.
 PR 06-AUG-1999; 99US-0147763P.

PR 27-JUL-2000; 2000US-00627897.
 XX (TIMA/) TIMANS J C.
 PA (PFLA/) PFLANZ S K.
 PA (KAST/) KASTELEIN R A.
 PA (BAZA/) BAZAN J F.
 XX Timans JC, Pflanz SK, Kastelein RA, Bazan JF;
 XX WPI; 2003-428883/40.
 DR N-PSDB; ACA61018.
 XX New substantially pure or isolated antigenic polypeptide that binds to
 PT the binding composition, useful for treating immune disorders, e.g. T-
 PT cell immune deficiencies, inflammation, tissue rejection, or
 PT cardiovascular conditions.
 XX Disclosure; Page 31-32; 39pp; English.
 XX The invention describes a substantially pure or isolated antigenic
 CC polypeptide, which binds to the binding composition comprising at least
 CC 17 contiguous amino acids from a sequence of 242, 231, 243 or 234 amino
 CC acids, fully defined in specification. The polynucleotides, polypeptides
 CC and antibodies are useful for regulating activation, development,
 CC differentiation, and functions of various cell types, including
 CC haematopoietic cells. They are also useful for treating abnormal medical
 CC conditions, including immune disorders, e.g. T-cell immune deficiencies,
 CC inflammation, tissue rejection, or cardiovascular or neurophysiological
 CC conditions. The antibodies are useful for detecting or diagnosing various
 CC immunological conditions related to expression of respective antigens.
 CC This is the amino acid sequence of human T-cell cytokine receptor (TCCR)
 CC to which the composite factor formed by IL-D80 and Epstein barr virus
 CC induced gene 3 (EB13) binds
 XX Sequence 636 AA;

Query Match 99.9%; Score 3494; DB 6; Length 636;
 Best Local Similarity 99.8%; Pred. No. 1.7e-264;
 Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRGGRGAPFWLWPKLALLPLLWVLFQRTTRPQSGAGPLQCYGVGGLDNCWSEPLGDL 60
 DB |||||
 QY 1 MRGGRGAPFWLWPKLALLPLLWVLFQRTTRPQSGAGPLQCYGVGGLDNCWSEPLGDL 60
 DB |||||
 QY 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPVPV 120
 DB |||||
 QY 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPVPV 120
 DB |||||
 QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHYRRCOEAAWTLLE 180
 DB |||||
 QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHYRRCOEAAWTLLE 180
 DB |||||
 QY 181 PELKTIPLTPVEIQDELEATGYKVCRCMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
 DB |||||
 QY 181 PELKTIPLTPVEIQDELEATGYKVCRCMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
 DB |||||
 QY 241 NLCGTPGGEPLLLWKAPGCVQVSKYKFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300
 DB |||||
 QY 241 NLCGTPGGEPLLLWKAPGCVQVSKYKFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300
 DB |||||
 QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVGGRELSPEGITCCCSLIPSGAEWARVSA 360
 DB |||||
 QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVGGRELSPEGITCCCSLIPSGAEWARVSA 360
 DB |||||
 QY 361 PLEKLNWVRLPGNLSALLPGNFTVGVYRITVAVSAGSLASASVWGFREELAPLVGP 420
 DB |||||
 QY 361 PLEKLNWVRLPGNLSALLPGNFTVGVYRITVAVSAGSLASASVWGFREELAPLVGP 420
 DB |||||
 QY 421 TLWRLQDAPPGTPTAANGVPRHQRHGLTHYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480
 DB |||||
 QY 421 TLWRLQDAPPGTPTAANGVPRHQRHGLTHYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480
 DB |||||
 QY 481 PWGPCELWVTASTIAGQGPPIRLHLPLDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
 DB |||||

Db 481 PWGCELVWVSTAGQPGPIRLRLHLPDNTLRKVLPGILFLWGLFLGCGSLATSG 540
 Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600
 Db 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600
 Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
 Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 10

ID ABG75880 standard; protein; 636 AA.

AC ABG75880;

DT 06-MAY-2003 (first entry)

XX Human interleukin-12 R beta 2 subunit homologue WSX-1/TCR.

XX Human; cytokine; IL-D80; IL-27; interleukin D80; interleukin 27;
 KW inflammation; autoimmune disorder; drug screening; cell activation;
 KW cell development; cell differentiation; WSX-1/TCR;
 KW interleukin-12 R beta 2 subunit.

XX Homo sapiens.

XX US2002164609-A1.

XX 07-NOV-2002.

XX 30-NOV-2001; 2001US-00000776.

XX 30-JUL-1999; 99US-0146581P.

XX 06-AUG-1999; 99US-0147763P.

XX 27-JUL-2000; 2000US-00627897.

XX 22-FEB-2001; 2001US-00791497.

XX (TIMA/) TIMANS J C.

XX (PFLA/) PFLANZ S K.

XX (KAST/) KASTELEIN R A.

XX (BAZA/) BAZAN J F.

XX (RENN/) RENNICK D.

XX (MALE/) DE WAAL MALEFYT R.

XX (CHEU/) CHEUNG J.

XX Timans JC, Pflanz SK, Kastelein RA, Bazan JF, Rennick D;

XX De Waal Malefyt R, Cheung J;

XX WPI; 2003-275305/27.

XX N-PSDB; ABX10922.

XX New isolated or recombinant cytokine or composite cytokine genes and
 PT proteins (e.g. interleukin D80 or interleukin 27), useful for diagnosing
 PT or treating e.g. inflammation or autoimmune disorders, or for regulating
 PT cell biology.

XX Claim 24; Page 30-32; 37pp; English.

XX The invention describes an isolated or recombinant polynucleotide, which
 CC encodes an antigenic polypeptide. The polynucleotide, polypeptide or
 CC binding compound is useful for diagnosing or treating IL-D80 or IL-27
 CC mediated conditions, e.g. inflammation or autoimmune disorders. These are
 CC also useful in drug screening. The polynucleotide, polypeptide,
 CC antibodies or compositions are also useful for controlling biology and
 CC physiology of mammalian cells (e.g. cells of a mammalian immune system),
 CC or for regulating the activation, development, differentiation, and
 CC function of various cell types (e.g. hematopoietic or lymphoid cells).
 CC This is the amino acid sequence of the human interleukin-12 R beta 2
 CC subunit homologue WSX-1/TCR used with human interleukin D80 (IL-D80) or
 CC 27 (IL-27) sequences to create a composite cytokine

XX SQ

Sequence 636 AA;

Query Match 99.9%; Score 3494; DB 6; Length 636;
 Best Local Similarity 99.8%; Pred. No. 1.7e-264;
 Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRGGRGAPFWLWPLKALPLLLWVLFQTRPQGSAGPLQCYGVGPIGLDNCSEPLGDL 60
 Db 1 MRGGRGAPFWLWPLKALPLLLWVLFQTRPQGSAGPLQCYGVGPIGLDNCSEPLGDL 60

Qy 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKQGPLWPPV 120
 Db 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKQGPLWPPV 120

Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
 Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180

Qy 181 PELKTIPLTPVEIQDLELATGYKYGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVVSG 240
 Db 181 PELKTIPLTPVEIQDLELATGYKYGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVVSG 240

Qy 241 NLCGTPGGEPLLLWKAPGCVQVYKVPFWGRELSPGEGITCCCSLIPSGAEWAVSA 300
 Db 241 NLCGTPGGEPLLLWKAPGCVQVYKVPFWGRELSPGEGITCCCSLIPSGAEWAVSA 300

Qy 301 VNATSWEPILNLSIVCLDSASAPRSVAVSSIASTELLVTWQPGEPLEHVVDWARDGD 360
 Db 301 VNATSWEPILNLSIVCLDSASAPRSVAVSSIASTELLVTWQPGEPLEHVVDWARDGD 360

Qy 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITTVAVSASGLASSVWGFREELAPLVGP 420
 Db 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITTVAVSASGLASSVWGFREELAPLVGP 420

Qy 421 TLWRLQDAPGTPAIANGVEPRHQLRHGLTHYLCAQSGTSPVCMVNSGNTQVTLPLDL 480
 Db 421 TLWRLQDAPGTPAIANGVEPRHQLRHGLTHYLCAQSGTSPVCMVNSGNTQVTLPLDL 480

Qy 481 PWGCELVWVSTAGQPGPIRLRLHLPDNTLRKVLPGILFLWGLFLGCGSLATSG 540
 Db 481 PWGCELVWVSTAGQPGPIRLRLHLPDNTLRKVLPGILFLWGLFLGCGSLATSG 540

Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600
 Db 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600

Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 11

AA29781

ID AAY29781 standard; protein; 636 AA.

XX AAY29781;

XX 04-NOV-1999 (first entry)

XX Human DNAX cytokine receptor subunit 1.

XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;

XX interleukin B30; DSR1; IL-B30; cytokine receptor; diagnosis;

XX inflammatory disorder; inflammatory response; innate immunity;

XX morphogenic development; immunological disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 108

XX /label= unknown

XX /note= "encoded by AYT"

XX WO9940195-A1.
 PN 12-AUG-1999.
 PD 05-FEB-1999; 99WO-US002600.
 PF 06-FEB-1998; 98US-0073941P.
 PR 13-MAY-1998; 98US-00078194.
 XX (SCHE) SCHERING CORP.
 PA Mattson JD, Mcclanahan TK, Kastelein RA;
 PI WPI: 1999-527306/44.
 DR N-PADB; AA208863.
 XX New receptor subunits useful in the treatment inflammatory disorders.
 PT Claim 2; Page 14-17; 133pp; English.
 PS The present invention describes a composition (I) comprising DNAX
 CC cytokine receptor subunit 1 (CDRS1) protein and DNAX soluble receptor
 CC subunit 1 (DSRS1) protein, which together encode a new mammalian cytokine
 CC related receptor (R), or CDRS1 and interleukin B30 (IL-B30) proteins, or
 CC DRS1 and IL-B30 proteins. (I) comprising DRS1 and CDRS1 is useful for
 CC screening for ligands (i.e. agonists/antagonists) from a library of
 CC compounds, which are useful for modulating the physiology or development
 CC of a cell or tissue culture e.g. inflammatory responses, innate immunity
 CC and/or morphogenic development. (R), antibodies and ligands are useful
 CC for treatment of conditions, especially immunological disorders,
 CC associated with conditions exhibiting abnormal expression of (R). (R) is
 CC useful as a phosphate labeling enzyme to label substrates, and the
 CC subunits DRS1 and CDRS1 are useful as immunogens for generating
 CC antibodies, or as antigens for binding antibodies. Nucleic acids encoding
 CC (R) are useful for identifying related DNAs and mRNAs, and variants from
 CC other individuals or species. The present sequence represents the
 CC specifically claimed human CDRS1, for use in the composition of the
 CC present invention
 XX Sequence 636 AA;
 SQ
 Query Match 99.8%; Score 3490; DB 2; Length 636;
 Best Local Similarity 99.7%; Pred. No. 3.4e-264;
 Matches 634; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRGGRGAPFWLWPKLALLLLVLFQRTTRQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
 DB 1 MRGGRGAPFWLWPKLALLLLVLFQRTTRQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
 QY 61 GAPSELHLOSQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPV 120
 DB 61 GAPSELHLOSQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTXKAGQPLWPPV 120
 QY 121 NLEQTMKNAPRLGPDVDFSEDDPLEATVHVAAPPTWPSHKVLICQFYHRCQEAATLLE 180
 DB 121 NLEQTMKNAPRLGPDVDFSEDDPLEATVHVAAPPTWPSHKVLICQFYHRCQEAATLLE 180
 QY 181 PELKTIPLTPVEIQDLIELATGVKRYGRMEKEEDLWGEWSPILSPQTTPSPAPKDVWSG 240
 DB 181 PELKTIPLTPVEIQDLIELATGVKRYGRMEKEEDLWGEWSPILSPQTTPSPAPKDVWSG 240
 QY 241 NLCGTPGGEEPLLWKAPGPCVQVSVKVMFWVGRELSPGEGITCCCSLIPSGAEARVSA 300
 DB 241 NLCGTPGGEEPLLWKAPGPCVQVSVKVMFWVGRELSPGEGITCCCSLIPSGAEARVSA 300
 QY 301 VNATSWEPITNLSVLCLDSASAPRSVAVSSVAGSTELLVTPQGPGEPLHVVWDWARDGD 360
 DB 301 VNATSWEPITNLSVLCLDSASAPRSVAVSSVAGSTELLVTPQGPGEPLHVVWDWARDGD 360
 QY 361 PLEKLNWRLPPGNLSALLPGNFTVGPYRITVAVSAGSLASASVWGFRELAPLVGP 420
 DB 361 PLEKLNWRLPPGNLSALLPGNFTVGPYRITVAVSAGSLASASVWGFRELAPLVGP 420

QY 421 TLWRLQDAPPCTPAIANGEVPRHQLRGLHLYTLCAQSGTSFVCMNVSGNTQSVTL 480
 DB 421 TLWRLQDAPPCTPAIANGEVPRHQLRGLHLYTLCAQSGTSFVCMNVSGNTQSVTL 480
 QY 481 PWGPCELWVTASTIAGQPPGPPIILRLHLPDNTLWKVLPGLFLWGLFLGCGLSLATSG 540
 DB 481 PWGPCELWVTASTIAGQPPGPPIILRLHLPDNTLWKVLPGLFLWGLFLGCGLSLATSG 540
 QY 541 RYHLRHVKVLPWWWEKVPDPANSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPVMESS 600
 DB 541 RYHLRHVKVLPWWWEKVPDPANSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPVMESS 600
 QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636
 DB 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636
 RESULT 12
 AAG65271
 ID AAG65271 standard; protein; 604 AA.
 AC AAG65271;
 XX 20-NOV-2001 (first entry)
 DT Cell factor receptor CRL1 related protein.
 DE Cell factor receptor CRL1 related protein.
 XX Cell factor receptor; CRL1; gpi30; cancer; inflammation;
 KW immunological rejection.
 XX Unidentified.
 OS CN1299828-A.
 PN 20-JUN-2001.
 PD 16-DEC-1999; 99CN-00124269.
 PF 16-DEC-1999; 99CN-00124269.
 PR 16-DEC-1999; 99CN-00124269.
 XX (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.
 PA Cao X, Zhang W, He L;
 PI WPI: 2001-523189/58.
 DR New cell factor acceptor, its code sequence and use.
 XX Example 1; Page 19; 27pp; Chinese.
 CC The present invention provides the protein and coding sequences of a
 CC novel cell factor receptor, designated CRL1. This is a homogeneous
 CC molecule of gpi30. The sequences can be used in the treatment of cancer,
 CC inflammation and immunological rejection. The present sequence is a
 CC protein described in the exemplification of the invention
 XX Sequence 604 AA;
 SQ
 Query Match 94.8%; Score 3316; DB 4; Length 604;
 Best Local Similarity 100.0%; Pred. No. 1.3e-250;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 QGSAGPLQCYGVGPGDLNCSWEPLGDLGAPSELHLOSQYRSNKTQTVAAAGRSWVAI 92
 DB 1 QGSAGPLQCYGVGPGDLNCSWEPLGDLGAPSELHLOSQYRSNKTQTVAAAGRSWVAI 60
 QY 93 PREQLTMSDKLLVWGTKAGQPLWPPVFNLETQMKPNAPRLGPDVDFSEDDPLEATVHVA 152
 DB 61 PREQLTMSDKLLVWGTKAGQPLWPPVFNLETQMKPNAPRLGPDVDFSEDDPLEATVHVA 120
 QY 153 PPTWESHKVLICQFYHRCQEAATLLEPELKIPLTPVEIQDLIELATGVKRYGRMEK 212

Db 121 PPTWPSHKVLICQPHYRRCQEAATLLEPELKTPIPTPVEIQDLELATGKYVGRCRMEX 180
QY 213 EEDLWGEWSPIILSFQTPPPAPKDVWSGNCIGTPGGREPLLWKAPGCPQVQVYKWFVW 272
Db 181 EEDLWGEWSPIILSFQTPPPAPKDVWSGNCIGTPGGREPLLWKAPGCPQVQVYKWFVW 240
QY 273 GRELSPGEGITCCCSLIPSGAEWARVSAVNATSWEPITNLSVCLDSASAPRSVAVSSIA 332
Db 241 GRELSPGEGITCCCSLIPSGAEWARVSAVNATSWEPITNLSVCLDSASAPRSVAVSSIA 300
QY 333 GSTELLVWQPGGEPLHVVWDARDGPLEKLNWVRLPGNLSALLPGNFTVGPYRIT 392
Db 301 GSTELLVWQPGGEPLHVVWDARDGPLEKLNWVRLPGNLSALLPGNFTVGPYRIT 360
QY 393 VTAVSASGLASASVWGFREELAPLVGPTLWRLQDAPPGTAPAWGEVPRHQLRGHLTHY 452
Db 361 VTAVSASGLASASVWGFREELAPLVGPTLWRLQDAPPGTAPAWGEVPRHQLRGHLTHY 420
QY 453 TLCAQSGTSPVCMVNSGNTQSVTLPLDPLWGPCELWWTASTIAGQGGPPGILRLHLPDNT 512
Db 421 TLCAQSGTSPVCMVNSGNTQSVTLPLDPLWGPCELWWTASTIAGQGGPPGILRLHLPDNT 480
QY 513 LRKWLPGILFLWGLFLGGLSLATSGRCYHLRHKVLPRWWEKYPDPANSSSGOPHME 572
Db 481 LRKWLPGILFLWGLFLGGLSLATSGRCYHLRHKVLPRWWEKYPDPANSSSGOPHME 540
QY 573 QVPEAQPLGDLPILEVEEMPPPPWMESSQPAQATAPLDSGYEKHFLPTPEELGLGPPRP 632
Db 541 QVPEAQPLGDLPILEVEEMPPPPWMESSQPAQATAPLDSGYEKHFLPTPEELGLGPPRP 600
QY 633 QVLA 636
Db 601 QVLA 604

RESULT 13
ABR41219
ID ABR41219 standard; protein; 680 AA.
XX
AC ABR41219;
XX
DT 02-JUN-2003 (first entry)
DE Human DITHP receptor.
XX
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging; receptor.
XX
OS Homo sapiens.
XX
PN WO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002WO-US010056.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX

PI Dafo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Doughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-129518/12.
DR N-PSDB; ACC46162.
XX
PT Novel human diagnostic and therapeutic polypeptide useful for identifying
PT test compound which specifically binds to a polypeptide encoded by human
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
PS Claim 27; SEQ ID NO 754; 591pp; English.
XX
CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which has receptor
CC activity. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 680 AA;
Query Match 94.0%; Score 3288; DB 6; Length 680;
Best Local Similarity 91.1%; Pred. No. 2.4e-248;
Matches 611; Conservative 3; Mismatches 21; Indels 36; Gaps 2;
QY 2 RGRGGAFFWMLPKLALLPL-----LWVLFQTRPGSAGPLQCYGVGLDLNCWSW 54
Db 10 RGRGTPCGEAGRPFLAVAAAGAAASVVGAFADASPAGSAGPLQCYGVGLDLNCWSW 69
QY 55 EPLGDLGAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLWVGTAKQPL 114
Db 70 EPLGDLGAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLWVGTAKQPL 129
QY 115 WPPVFVNLETQ-----MKPNAPRLGPDVDFSEDDPL 145
Db 130 WPPVFVNLETQSNVAGGWALYAGVLLGVVHVTLSVSPKPNAPRLGPDVDFSEDDPL 189
QY 146 EATVHWAPTPWPSHKVLICQPHYRRCQEAATLLEPELKTPIPTPVEIQDLELATGKYV 205
Db 190 EATVHWAPTPWPSHKVLICQPHYRRCQEAATLLEPELKTPIPTPVEIQDLELATGKYV 249
QY 206 GRCRMEKEEDLWGEWSPIILSFQTPPPAPKDVWSGNCIGTPGGREPLLWKAPGCPQVQS 265
Db 250 GRCRMEKEEDLWGEWSPIILSFQTPPPAPKDVWSGNCIGTPGGREPLLWKAPGCPQVQS 309
QY 266 YKWFVWVGRELSPEGITCCCSLIPSGAEWARVSAVNATSWEPITNLSVCLDSASAPRS 325
XX

Db 310 YKWFVWVGRELSPGEGITCCSILIPSGAEWAVSAVNATSWEBLTLNLSLVCLDSASAPRS 369
 QY 326 VAVSSIAGSTELLVTWQPGPGPLEHVVDWADGDPLEKLNWRLPPGNLSALLPGNFV 385
 Db 370 VAVSSIAGSTELLVTWQPGPGPLEHVVDWADGDPLEKLNWRLPPGNLSALLPGNFV 429
 QY 386 GVPYRITVTAVSAGSLASASSVWGPREEELAPLVGPTLWRLQDAPGCTPAIANGVEPRHQL 445
 Db 430 GVPYRITVTAVSAGSLASASSVWGPREEELAPLVGPTLWRLQDAPGCTPAIANGVEPRHQL 489
 QY 446 RGHLYTLCAQSGTSPSVMNVSGNTQSVTLPLDPWGPCELVWVASTIAGQPGPIIL 505
 Db 490 RGHLYTLCAQSGTSPSVMNVSGNTQSVTLPLDPWGPCELVWVASTIAGQPGPIIL 549
 QY 506 LHLPTNLTNRKVLPGILLFLWGLFLICGGLSLATSGRCYHLRHKVLPRWWEKVPDPANSS 565
 Db 550 LHLPTNLTNRKVLPGILLFLWGLFLICGGLSLATSGRCYHLRHKVLPRWWEKVPDPANSS 609
 QY 566 SGQPMQEVPEAQLDGLDLPILVEEMEPVPMVMESSQPAQATAPLDSGYEKHFLPTPEELG 625
 Db 610 SGQPMQEVPEAQLDGLDLPILVEEMEPVPMVMESSQPAQATAPLDSGYEKHFLPTPEELG 669
 QY 626 LLGPPRPQVLA 636
 Db 670 LLGPPRPQVLA 680

RESULT 14

ID AAW33398
 XX AAW33398 standard; protein; 578 AA.
 AC AAW33398;
 DT 22-MAY-1998 (first entry)
 DE Human haematopoietic cytokine receptor Zcytor1.
 KW Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;
 KW cancer diagnosis; agonist; antagonist.
 XX Homo sapiens.
 OS WO9744455-A1.
 XX 27-NOV-1997.
 PD 19-MAY-1997; 97MO-US008502.
 PF 23-MAY-1996; 96US-00653740.
 PR (ZYMO) ZYMOGENETICS INC.
 PA Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
 PI WPI: 1998-018509/02.
 DR N-PSDB; AAT94119.
 XX Haematopoietic cytokine receptor - useful for ligand detection, and
 PT pathological condition diagnosis.
 PS Claim 1; Page 39-43; 86pp; English.
 XX The present sequence is the human haematopoietic cytokine receptor
 CC Zcytor1, useful for ligand detection, and pathological condition
 CC diagnosis, including cancer. Receptor agonists of the protein can be used
 CC to stimulate the proliferation and development of target cells in vitro
 CC and in vivo. The agonists can stimulate cell mediated immunity and
 CC lymphocyte proliferation, to treat infection involving immunosuppression,
 CC e.g. viral infections. They may also be used to suppress tumours, induce
 CC cytotoxicity, treat leukaemias and enhance the regeneration of the T-
 CC cell repertoire after bone marrow transplantation. Antagonists of the
 CC protein may be used to suppress the immune system, treat autoimmune
 CC diseases, including rheumatoid arthritis, multiple sclerosis and diabetes

CC mellitis. Immune suppression caused by the antagonists can also be used
 CC to reduce rejection of tissue or organ transplants and grafts, and to
 XX treat T-cell specific leukaemias and lymphomas
 SQ Sequence 578 AA;
 Query Match 90.1%; Score 3150; DB 2; Length 578;
 Best Local Similarity 90.9%; Pred. No. 1.2e-237;
 Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;
 QY 1 MRGRGAPFWLWPLPKALLPLLVLFORTRPGSAGPLQCYGVGPGDLNCSWPLDGL 60
 Db 1 MRGRGAPFWLWPLPKALLPLLVLFORTRPGSAGPLQCYGVGPGDLNCSWPLDGL 60
 QY 61 GAPSELHLOSQKYSRNTQTQTVAAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPVPFV 120
 Db 61 GAPSELHLOSQKYSRNTQTQTVAAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPVPFV 120
 QY 121 NLETQMKENAPRLGPDVDFSEDDPLEATVHWAPTPSHKVLICQFHYRRCOEAAWTLLE 180
 Db 121 NLETQMKENAPRLGPDVDFSEDDPLEATVHWAPTPSHKVLICQFHYRRCOEAAWTLLE 180
 QY 181 PELKTIPLTPVEIODLELATGKVVGRCKMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
 Db 181 PELKTIPLTPVEIODLELATGKVVGRCKMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
 QY 241 NLGCTPGGEEPLLWKAAPGCVQVSYKVFVWVGRELSPEGITCCCSLIPSGAEWAVSA 300
 Db 241 NLGCTPGGEEPLLWKAAPGCVQVSYKVFVWVGRELSPEGITCCCSLIPSGAEWAVSA 300
 QY 301 VNATSWEPFLNLSVCLDSASAPRSVAVSSITAGSTELLVTWQPGPELEHVVDWADGD 360
 Db 301 VNATSWEPFLNLSVCLDSASAPRSVAVSSITAGSTELLVTWQPGPELEHVVDWADGD 360
 QY 361 PLEKLNWRLPPLNLSALLPGNFVTVAVSAGSLASASSVWGPREEELAPLVGP 420
 Db 361 PLEKLNWRLPPLNLSALLPGNFVTVAVSAGSLASASSVWGPREEELAPLVGP 420
 QY 421 TLWRLQDAPGCTPAIANGVEPRHQLRHLTHYTLCAQSGTSPSVMNVSGNTQSVTLPLD 480
 Db 421 TLWRLQDAPGCTPAIANGVEPRHQLRHLTHYTLCAQSGTSPSVMNVSGNTQSVTLPLD 480
 QY 481 PWGPCELVWVASTIAGQPGPIILRLHLPDNTLRKVLPGILLFLWGLFLICGGLSLATSG 540
 Db 481 PWGPCELVWVASTIAGQPGPIILRLHLPDNTLRKVLPGILLFLWGLFLICGGLSLATSG 540
 QY 541 RCYHLRHKVLPRWWEKVPDPANSSSQPHMEQVPEAQLDGLDLPILVEEMEPVPMVMESS 600
 Db 541 RCYHLRHKVLPRWWEKVPDPANSSSQPHMEQVPEAQLDGLDLPILVEEMEPVPMVMESS 600
 QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636
 Db 567 -----GLLGPPRPQVLA 578
 RESULT 15
 ADO26826
 ID ADO26826 standard; protein; 558 AA.
 XX ADO26826;
 AC ADO26826;
 DT 12-AUG-2004 (first entry)
 DE Human receptors and membrane-associated protein, REMAP-16.
 KW Human; receptors and membrane-associated protein; REMAP;
 KW cell proliferative disorder; autoimmune disorder; inflammatory disorder;
 KW neurological disorder; infection; developmental disorder;
 KW nervous system disorder; mental disorder; metabolic disorder;
 KW hepatotropic; antiparotatic; neurotropic; neuroprotective;
 KW antiparkinsonian; anticonvulsant; anorectic; osteopathic;
 KW hypertensive; anti-HIV; antiaesthetic; antianaemic; ophthalmological;
 KW thrombolytic; anticoagulant.

XX	Homo sapiens.	
OS	WO2004044159-A2.	
XX	27-MAY-2004.	
XX	10-NOV-2003; 2003WO-US035752.	
XX	12-NOV-2002; 2002US-0425404P.	
PR	15-JAN-2003; 2003US-0440907P.	
PR	24-JAN-2003; 2003US-0442477P.	
PR	18-FEB-2003; 2003US-0448565P.	
PR	04-APR-2003; 2003US-0460716P.	
PR	09-APR-2003; 2003US-0461853P.	
XX	(INCY-) INCYTE CORP.	
XX	Lee SY, Swarnakar A, Murage J, Khare R, Hafalia AJA, Chawla NK; PI Elliott VS, Tran UK, Becha SD, Bhatia U, Burrill JD, Lee S; PI Blake JJ, Ho A, Zheng W, Marquis JP, Jin P, Wilson AD, Wang JT; PI Chien D, Richardson TW, Kable AE, Emerling BM, Ramkumar J; PI Baughn MR, Tang YT, Jackson JL, Lal PG, Yue H, Gietzen KJ; XX WPI; 2004-420303/39. DR N-PSDB; ADO26875. XX	223 VNATSWEP LTNLSVLCDSASAPRSVAVSSVAGSTELLVSWQPGPGEPLVHVVDWARDGD 282
XX	Novel isolated human receptors and membrane-associated proteins, REMAP 1- PT 49, useful for diagnosing, treating, preventing AIDS, obesity, PT hypothyroidism, acromegaly, cataract, thrombosis, Alzheimer's disease. XX	361 PLEKLNWVRLPPCGNLGALLPGNFTVGVYRITVTAVSASGLASASSVWGFREELAPLVGP 420
XX	Claim 1; SEQ ID NO 16; 292pp; English.	283 PLEKLNWVRLPPCGNLGALLPGNFTVGVYRITVTAVSASGLASASSVWGFREELAPLVGP 342
XX	The present invention relates to the isolation of human receptors and CC membrane-associated proteins (REMAP, designated REMAP-1 to REMAP-49), and CC the polynucleotide sequences encoding them. Also disclosed are expression CC vectors, host cells, antibodies, agonists, and antagonists. The CC polypeptide and polynucleotide sequences of the invention are useful for CC diagnosing, treating, and preventing disorders associated with aberrant CC expression of REMAP. Such disorders include cell proliferative disorders, CC autoimmune disorders, inflammatory disorders, neurological disorders, CC infections, developmental disorders, nervous system disorders, mental CC disorders, metabolic disorders etc. The present sequence represents a CC REMAP polypeptide of the invention. XX	421 TLMRLQDAPPGTPTAIANGEVPRHQLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL 480
SQ	Sequence 558 AA;	343 TLMRLQDAPPGTPTAIANGEVPRHQLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL 402

Search completed: February 19, 2005, 01:12:54
Job time : 179 secs

XX	Query Match	86.0%; Score 3007; DB 8; Length 558;
XX	Best Local Similarity	87.4%; Pred. No. 1.9e-226;
XX	Matches	556; Conservative 1; Mismatches 1; Indels 78; Gaps 1;
Qy	1 MRGGRGAPFWLWPLPKLALLPLLVLFORTPOGSAGPLQCYGVGLDNCSEWPLGDL 60	
Db	1 MRGGRGAPFWLWPLPKLALLPLLVLFORTPOGSAGPLQCYGVGLDNCSEWPLGDL 60	
Qy	61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVMGTGKAGQPLWPPFV 120	
Db	61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVMGTGKAGQPLWPPFV 120	
Qy	121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAANTLLE 180	
Db	121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAANTLLE 178	
Qy	181 PELKTIPLTPVEIQDLATGYKYVGRCKEEDLWGEWSPILSFQTTPSAPKDVWVSG 240	
Db	179 ----- 178	
Qy	241 NLCGTPGGEPELLWKPAPCVQVSYKVFVWVGRELSPEGITCCCSLIPSGAEWARVSA 300	
Db	179 -----APGPCVQVSYKVFVWVGRELSPEGITCCCSLIPSGAEWARVSA 222	
Qy	301 VNATSWEP LTNLSVLCDSASAPRSVAVSSVAGSTELLVWQPGPGEPLVHVVDWARDGD 360	

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